



RECEIVED

DEC 26 2001

TECH CENTER 1600/2900

SEQUENCE LISTING

<110> ARNOLD, Frances H.
PETROUNIA, Ionna P.
SUN, Lianhong

<120> DIRECTED EVOLUTION OF OXIDASE ENZYMES

<130> 9373/1G811US1

<140> 09/722,602

<141> 2000-11-27

<150> US 09/571,553

<151> 2000-05-16

<160> 48

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 1

aB aattcgaagc ttatggcctc agcacctatc ggaagc

36

<210> 2

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 2

cttccttcta gattactgag taacgcgaat cgt

33

<210> 3

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 3

ggaagagaat tcaatacgca aaccgcctct	30
<p><210> 4</p> <p><211> 32</p> <p><212> DNA</p> <p><213> Artificial Sequence</p> <p><220></p> <p><223> Primer</p>	
ggtcataagc ttttcctgtg tgaaattggt at	32
<p><210> 5</p> <p><211> 30</p> <p><212> DNA</p> <p><213> Artificial Sequence</p> <p><220></p> <p><223> Primer</p>	
accatgattt cgacgtcggc accctcagca	30
<p><210> 6</p> <p><211> 30</p> <p><212> DNA</p> <p><213> Artificial Sequence</p> <p><220></p> <p><223> Primer</p>	
cttcctaagc tttcactgag taacgcgaat	30
<p><210> 7</p> <p><211> 30</p> <p><212> DNA</p> <p><213> Artificial Sequence</p> <p><220></p> <p><223> Primer</p>	
ggaagaggta ccaatacgca aaccgcctct	30
<p><210> 8</p> <p><211> 29</p> <p><212> DNA</p> <p><213> Artificial Sequence</p> <p><220></p> <p><223> Primer</p>	

<400> 8
 ttgttcctgc ggctgcagca attgaaccg

29

<210> 9
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 9
 tgccggtcga ctctagatta ctgagtaacg

30

<210> 10
 <211> 639
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Mutant 9.16.8D2 (N537D) of D. dendroides GaO

<400> 10
 Ala Ser Ala Pro Ile Gly Ser Ala Ile Ser Arg Asn Asn Trp Ala Val
 1 5 10 15
 Thr Cys Asp Ser Ala Gln Ser Gly Asn Glu Cys Asn Lys Ala Ile Asp
 20 25 30
 Gly Asn Lys Asp Thr Phe Trp His Thr Phe Tyr Gly Ala Asn Gly Asp
 35 40 45
 Pro Lys Pro Pro His Thr Tyr Thr Ile Asp Met Lys Thr Thr Gln Asn
 50 55 60
 Val Asn Gly Leu Ser Met Leu Pro Arg Gln Asp Gly Asn Gln Asn Gly
 65 70 75 80
 Trp Ile Gly Arg His Glu Val Tyr Leu Ser Ser Asp Gly Thr Asn Trp
 85 90 95
 Gly Ser Pro Val Ala Ser Gly Ser Trp Phe Ala Asp Ser Thr Thr Lys
 100 105 110
 Tyr Ser Asn Phe Glu Thr Arg Pro Ala Arg Tyr Val Arg Leu Val Ala
 115 120 125
 Ile Thr Glu Ala Asn Gly Gln Pro Trp Thr Ser Ile Ala Glu Ile Asn
 130 135 140
 Val Phe Gln Ala Ser Ser Tyr Thr Ala Pro Gln Pro Gly Leu Gly Arg
 145 150 155 160
 Trp Gly Pro Thr Ile Asp Leu Pro Ile Val Pro Ala Ala Ala Ala Ile
 165 170 175
 Glu Pro Thr Ser Gly Arg Val Leu Met Trp Ser Ser Tyr Arg Asn Asp
 180 185 190
 Ala Phe Gly Gly Ser Pro Gly Gly Ile Thr Leu Thr Ser Ser Trp Asp
 195 200 205
 Pro Ser Thr Gly Ile Val Ser Asp Arg Thr Val Thr Val Thr Lys His
 210 215 220
 Asp Met Phe Cys Pro Gly Ile Ser Met Asp Gly Asn Gly Gln Ile Val

225	Val	Thr	Gly	Gly	Asn	Asp	Ala	Lys	Lys	Thr	Ser	Leu	Tyr	Asp	Ser	Ser
					245					250					255	
Ser	Asp	Ser	Trp	Ile	Pro	Gly	Pro	Asp	Met	Gln	Val	Ala	Arg	Gly	Tyr	
			260					265					270			
Gln	Ser	Ser	Ala	Thr	Met	Ser	Asp	Gly	Arg	Val	Phe	Thr	Ile	Gly	Gly	
		275					280				285					
Ser	Trp	Ser	Gly	Gly	Val	Phe	Glu	Lys	Asn	Gly	Glu	Val	Tyr	Ser	Pro	
	290					295					300					
Ser	Ser	Lys	Thr	Trp	Thr	Ser	Leu	Pro	Asn	Ala	Lys	Val	Asn	Pro	Met	
305					310					315					320	
Leu	Thr	Ala	Asp	Lys	Gln	Gly	Leu	Tyr	Arg	Ser	Asp	Asn	His	Ala	Trp	
				325					330					335		
Leu	Phe	Gly	Trp	Lys	Lys	Gly	Ser	Val	Phe	Gln	Ala	Gly	Pro	Ser	Thr	
			340					345					350			
Ala	Met	Asn	Trp	Tyr	Tyr	Thr	Ser	Gly	Ser	Gly	Asp	Val	Lys	Ser	Ala	
		355					360					365				
Gly	Lys	Arg	Gln	Ser	Asn	Arg	Gly	Val	Ala	Pro	Asp	Ala	Met	Cys	Gly	
	370					375					380					
Asn	Ala	Val	Met	Tyr	Asp	Ala	Val	Lys	Gly	Lys	Ile	Leu	Thr	Phe	Gly	
385					390					395					400	
Gly	Ser	Pro	Asp	Tyr	Gln	Asp	Ser	Asp	Ala	Thr	Thr	Asn	Ala	His	Ile	
				405					410					415		
Ile	Thr	Leu	Gly	Glu	Pro	Gly	Thr	Ser	Pro	Asn	Thr	Val	Phe	Ala	Ser	
			420					425					430			
Asn	Gly	Leu	Tyr	Phe	Ala	Arg	Thr	Phe	His	Thr	Ser	Val	Val	Leu	Pro	
		435					440					445				
Asp	Gly	Ser	Thr	Phe	Ile	Thr	Gly	Gly	Gln	Arg	Arg	Gly	Ile	Pro	Phe	
	450					455					460					
Glu	Asp	Ser	Thr	Pro	Val	Phe	Thr	Pro	Glu	Ile	Tyr	Val	Pro	Glu	Gln	
465					470					475					480	
Asp	Thr	Phe	Tyr	Lys	Gln	Asn	Pro	Asn	Ser	Ile	Val	Arg	Val	Tyr	His	
				485					490					495		
Ser	Ile	Ser	Leu	Leu	Pro	Asp	Gly	Arg	Val	Phe	Asn	Gly	Gly	Gly		
			500				505					510				
Gly	Leu	Cys	Gly	Asp	Cys	Thr	Thr	Asn	His	Phe	Asp	Ala	Gln	Ile	Phe	
		515					520					525				
Thr	Pro	Asn	Tyr	Leu	Tyr	Asn	Ser	Asp	Gly	Asn	Leu	Ala	Thr	Arg	Pro	
	530					535					540					
Lys	Ile	Thr	Arg	Thr	Ser	Thr	Gln	Ser	Val	Lys	Val	Gly	Gly	Arg	Ile	
545					550					555					560	
Thr	Ile	Ser	Thr	Asp	Ser	Ser	Ile	Ser	Lys	Ala	Ser	Leu	Ile	Arg	Tyr	
				565					570					575		
Gly	Thr	Ala	Thr	His	Thr	Val	Asn	Thr	Asp	Gln	Arg	Arg	Ile	Pro	Leu	
			580					585					590			
Thr	Leu	Thr	Asn	Asn	Gly	Gly	Asn	Ser	Tyr	Ser	Phe	Gln	Val	Pro	Ser	
		595					600					605				
Asp	Ser	Gly	Val	Ala	Leu	Pro	Gly	Tyr	Trp	Met	Leu	Phe	Val	Met	Asn	
	610					615					620					
Ser	Ala	Gly	Val	Pro	Ser	Val	Ala	Ser	Thr	Ile	Arg	Val	Thr	Gln		
625					630					635						

<211> 639
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Mutant 9.16.6C11 (V494A, C515S) of D. dendroides
 GaO

<400> 11

Ala	Ser	Ala	Pro	Ile	Gly	Ser	Ala	Ile	Ser	Arg	Asn	Asn	Trp	Ala	Val
1				5					10					15	
Thr	Cys	Asp	Ser	Ala	Gln	Ser	Gly	Asn	Glu	Cys	Asn	Lys	Ala	Ile	Asp
			20					25					30		
Gly	Asn	Lys	Asp	Thr	Phe	Trp	His	Thr	Phe	Tyr	Gly	Ala	Asn	Gly	Asp
		35					40					45			
Pro	Lys	Pro	Pro	His	Thr	Tyr	Thr	Ile	Asp	Met	Lys	Thr	Thr	Gln	Asn
	50					55					60				
Val	Asn	Gly	Leu	Ser	Met	Leu	Pro	Arg	Gln	Asp	Gly	Asn	Gln	Asn	Gly
65					70					75					80
Trp	Ile	Gly	Arg	His	Glu	Val	Tyr	Leu	Ser	Ser	Asp	Gly	Thr	Asn	Trp
				85					90					95	
Gly	Ser	Pro	Val	Ala	Ser	Gly	Ser	Trp	Phe	Ala	Asp	Ser	Thr	Thr	Lys
			100					105					110		
Tyr	Ser	Asn	Phe	Glu	Thr	Arg	Pro	Ala	Arg	Tyr	Val	Arg	Leu	Val	Ala
		115					120					125			
Ile	Thr	Glu	Ala	Asn	Gly	Gln	Pro	Trp	Thr	Ser	Ile	Ala	Glu	Ile	Asn
	130					135					140				
Val	Phe	Gln	Ala	Ser	Ser	Tyr	Thr	Ala	Pro	Gln	Pro	Gly	Leu	Gly	Arg
145					150					155					160
Trp	Gly	Pro	Thr	Ile	Asp	Leu	Pro	Ile	Val	Pro	Ala	Ala	Ala	Ala	Ile
				165					170					175	
Glu	Pro	Thr	Ser	Gly	Arg	Val	Leu	Met	Trp	Ser	Ser	Tyr	Arg	Asn	Asp
			180					185					190		
Ala	Phe	Gly	Gly	Ser	Pro	Gly	Gly	Ile	Thr	Leu	Thr	Ser	Ser	Trp	Asp
		195					200					205			
Pro	Ser	Thr	Gly	Ile	Val	Ser	Asp	Arg	Thr	Val	Thr	Val	Thr	Lys	His
	210					215					220				
Asp	Met	Phe	Cys	Pro	Gly	Ile	Ser	Met	Asp	Gly	Asn	Gly	Gln	Ile	Val
225					230					235					240
Val	Thr	Gly	Gly	Asn	Asp	Ala	Lys	Lys	Thr	Ser	Leu	Tyr	Asp	Ser	Ser
				245					250					255	
Ser	Asp	Ser	Trp	Ile	Pro	Gly	Pro	Asp	Met	Gln	Val	Ala	Arg	Gly	Tyr
			260					265					270		
Gln	Ser	Ser	Ala	Thr	Met	Ser	Asp	Gly	Arg	Val	Phe	Thr	Ile	Gly	Gly
		275					280					285			
Ser	Trp	Ser	Gly	Gly	Val	Phe	Glu	Lys	Asn	Gly	Glu	Val	Tyr	Ser	Pro
	290					295					300				
Ser	Ser	Lys	Thr	Trp	Thr	Ser	Leu	Pro	Asn	Ala	Lys	Val	Asn	Pro	Met
305					310					315					320
Leu	Thr	Ala	Asp	Lys	Gln	Gly	Leu	Tyr	Arg	Ser	Asp	Asn	His	Ala	Trp
				325					330					335	
Leu	Phe	Gly	Trp	Lys	Lys	Gly	Ser	Val	Phe	Gln	Ala	Gly	Pro	Ser	Thr
			340					345					350		

Ala	Met	Asn	Trp	Tyr	Tyr	Thr	Ser	Gly	Ser	Gly	Asp	Val	Lys	Ser	Ala
		355					360					365			
Gly	Lys	Arg	Gln	Ser	Asn	Arg	Gly	Val	Ala	Pro	Asp	Ala	Met	Cys	Gly
	370					375					380				
Asn	Ala	Val	Met	Tyr	Asp	Ala	Val	Lys	Gly	Lys	Ile	Leu	Thr	Phe	Gly
385					390					395					400
Gly	Ser	Pro	Asp	Tyr	Gln	Asp	Ser	Asp	Ala	Thr	Thr	Asn	Ala	His	Ile
			405					410						415	
Ile	Thr	Leu	Gly	Glu	Pro	Gly	Thr	Ser	Pro	Asn	Thr	Val	Phe	Ala	Ser
		420						425					430		
Asn	Gly	Leu	Tyr	Phe	Ala	Arg	Thr	Phe	His	Thr	Ser	Val	Val	Leu	Pro
	435						440					445			
Asp	Gly	Ser	Thr	Phe	Ile	Thr	Gly	Gly	Gln	Arg	Arg	Gly	Ile	Pro	Phe
	450					455					460				
Glu	Asp	Ser	Thr	Pro	Val	Phe	Thr	Pro	Glu	Ile	Tyr	Val	Pro	Glu	Gln
465					470					475					480
Asp	Thr	Phe	Tyr	Lys	Gln	Asn	Pro	Asn	Ser	Ile	Val	Arg	Ala	Tyr	His
			485					490						495	
Ser	Ile	Ser	Leu	Leu	Leu	Pro	Asp	Gly	Arg	Val	Phe	Asn	Gly	Gly	Gly
		500						505					510		
Gly	Leu	Ser	Gly	Asp	Cys	Thr	Thr	Asn	His	Phe	Asp	Ala	Gln	Ile	Phe
	515						520					525			
Thr	Pro	Asn	Tyr	Leu	Tyr	Asn	Ser	Asn	Gly	Asn	Leu	Ala	Thr	Arg	Pro
	530					535					540				
Lys	Ile	Thr	Arg	Thr	Ser	Thr	Gln	Ser	Val	Lys	Val	Gly	Gly	Arg	Ile
545					550					555					560
Thr	Ile	Ser	Thr	Asp	Ser	Ser	Ile	Ser	Lys	Ala	Ser	Leu	Ile	Arg	Tyr
			565					570						575	
Gly	Thr	Ala	Thr	His	Thr	Val	Asn	Thr	Asp	Gln	Arg	Arg	Ile	Pro	Leu
		580						585					590		
Thr	Leu	Thr	Asn	Asn	Gly	Gly	Asn	Ser	Tyr	Ser	Phe	Gln	Val	Pro	Ser
	595						600					605			
Asp	Ser	Gly	Val	Ala	Leu	Pro	Gly	Tyr	Trp	Met	Leu	Phe	Val	Met	Asn
	610					615					620				
Ser	Ala	Gly	Val	Pro	Ser	Val	Ala	Ser	Thr	Ile	Arg	Val	Thr	Gln	
625					630					635					

<210> 12
 <211> 639
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Mutant 9.16.16D12 (P136, V494A) of D. dendroides
 GaO

<400> 12															
Ala	Ser	Ala	Pro	Ile	Gly	Ser	Ala	Ile	Ser	Arg	Asn	Asn	Trp	Ala	Val
1				5				10					15		
Thr	Cys	Asp	Ser	Ala	Gln	Ser	Gly	Asn	Glu	Cys	Asn	Lys	Ala	Ile	Asp
			20					25					30		
Gly	Asn	Lys	Asp	Thr	Phe	Trp	His	Thr	Phe	Tyr	Gly	Ala	Asn	Gly	Asp
	35						40						45		

Pro	Lys	Pro	Pro	His	Thr	Tyr	Thr	Ile	Asp	Met	Lys	Thr	Thr	Gln	Asn
50						55					60				
Val	Asn	Gly	Leu	Ser	Met	Leu	Pro	Arg	Gln	Asp	Gly	Asn	Gln	Asn	Gly
65					70					75					80
Trp	Ile	Gly	Arg	His	Glu	Val	Tyr	Leu	Ser	Ser	Asp	Gly	Thr	Asn	Trp
				85					90					95	
Gly	Ser	Pro	Val	Ala	Ser	Gly	Ser	Trp	Phe	Ala	Asp	Ser	Thr	Thr	Lys
			100					105					110		
Tyr	Ser	Asn	Phe	Glu	Thr	Arg	Pro	Ala	Arg	Tyr	Val	Arg	Leu	Val	Ala
		115					120					125			
Ile	Thr	Glu	Ala	Asn	Gly	Gln	Pro	Trp	Thr	Ser	Ile	Ala	Glu	Ile	Asn
	130					135					140				
Val	Phe	Gln	Ala	Ser	Ser	Tyr	Thr	Ala	Pro	Gln	Pro	Gly	Leu	Gly	Arg
145					150					155					160
Trp	Gly	Pro	Thr	Ile	Asp	Leu	Pro	Ile	Val	Pro	Ala	Ala	Ala	Ala	Ile
				165					170					175	
Glu	Pro	Thr	Ser	Gly	Arg	Val	Leu	Met	Trp	Ser	Ser	Tyr	Arg	Asn	Asp
			180					185					190		
Ala	Phe	Gly	Gly	Ser	Pro	Gly	Gly	Ile	Thr	Leu	Thr	Ser	Ser	Trp	Asp
	195					200						205			
Pro	Ser	Thr	Gly	Ile	Val	Ser	Asp	Arg	Thr	Val	Thr	Val	Thr	Lys	His
	210					215					220				
Asp	Met	Phe	Cys	Pro	Gly	Ile	Ser	Met	Asp	Gly	Asn	Gly	Gln	Ile	Val
225					230					235					240
Val	Thr	Gly	Gly	Asn	Asp	Ala	Lys	Lys	Thr	Ser	Leu	Tyr	Asp	Ser	Ser
				245					250					255	
Ser	Asp	Ser	Trp	Ile	Pro	Gly	Pro	Asp	Met	Gln	Val	Ala	Arg	Gly	Tyr
			260					265					270		
Gln	Ser	Ser	Ala	Thr	Met	Ser	Asp	Gly	Arg	Val	Phe	Thr	Ile	Gly	Gly
	275						280					285			
Ser	Trp	Ser	Gly	Gly	Val	Phe	Glu	Lys	Asn	Gly	Glu	Val	Tyr	Ser	Pro
	290					295				300					
Ser	Ser	Lys	Thr	Trp	Thr	Ser	Leu	Pro	Asn	Ala	Lys	Val	Asn	Pro	Met
305					310					315					320
Leu	Thr	Ala	Asp	Lys	Gln	Gly	Leu	Tyr	Arg	Ser	Asp	Asn	His	Ala	Trp
				325					330					335	
Leu	Phe	Gly	Trp	Lys	Lys	Gly	Ser	Val	Phe	Gln	Ala	Gly	Pro	Ser	Thr
			340					345					350		
Ala	Met	Asn	Trp	Tyr	Tyr	Thr	Ser	Gly	Ser	Gly	Asp	Val	Lys	Ser	Ala
		355					360					365			
Gly	Lys	Arg	Gln	Ser	Asn	Arg	Gly	Val	Ala	Pro	Asp	Ala	Met	Cys	Gly
	370					375					380				
Asn	Ala	Val	Met	Tyr	Asp	Ala	Val	Lys	Gly	Lys	Ile	Leu	Thr	Phe	Gly
385					390					395					400
Gly	Ser	Pro	Asp	Tyr	Gln	Asp	Ser	Asp	Ala	Thr	Thr	Asn	Ala	His	Ile
				405					410					415	
Ile	Thr	Leu	Gly	Glu	Pro	Gly	Thr	Ser	Pro	Asn	Thr	Val	Phe	Ala	Ser
			420					425					430		
Asn	Gly	Leu	Tyr	Phe	Ala	Arg	Thr	Phe	His	Thr	Ser	Val	Val	Leu	Pro
		435					440					445			
Asp	Gly	Ser	Thr	Phe	Ile	Thr	Gly	Gly	Gln	Arg	Arg	Gly	Ile	Pro	Phe
	450					455					460				
Glu	Asp	Ser	Thr	Pro	Val	Phe	Thr	Pro	Glu	Ile	Tyr	Val	Pro	Glu	Gln

465					470					475					480
Asp	Thr	Phe	Tyr	Lys	Gln	Asn	Pro	Asn	Ser	Ile	Val	Arg	Ala	Tyr	His
				485					490					495	
Ser	Ile	Ser	Leu	Leu	Leu	Pro	Asp	Gly	Arg	Val	Phe	Asn	Gly	Gly	Gly
			500					505					510		
Gly	Leu	Cys	Gly	Asp	Cys	Thr	Thr	Asn	His	Phe	Asp	Ala	Gln	Ile	Phe
		515					520					525			
Thr	Pro	Asn	Tyr	Leu	Tyr	Asn	Ser	Asn	Gly	Asn	Leu	Ala	Thr	Arg	Pro
	530					535					540				
Lys	Ile	Thr	Arg	Thr	Ser	Thr	Gln	Ser	Val	Lys	Val	Gly	Gly	Arg	Ile
545					550					555					560
Thr	Ile	Ser	Thr	Asp	Ser	Ser	Ile	Ser	Lys	Ala	Ser	Leu	Ile	Arg	Tyr
				565					570					575	
Gly	Thr	Ala	Thr	His	Thr	Val	Asn	Thr	Asp	Gln	Arg	Arg	Ile	Pro	Leu
			580					585					590		
Thr	Leu	Thr	Asn	Asn	Gly	Gly	Asn	Ser	Tyr	Ser	Phe	Gln	Val	Pro	Ser
		595					600					605			
Asp	Ser	Gly	Val	Ala	Leu	Pro	Gly	Tyr	Trp	Met	Leu	Phe	Val	Met	Asn
	610					615					620				
Ser	Ala	Gly	Val	Pro	Ser	Val	Ala	Ser	Thr	Ile	Arg	Val	Thr	Gln	
625					630					635					

<210> 13
 <211> 639
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Mutant 11.03.6D3 (S10P, P136, V494A) of D.
 dendroides GaO

<400> 13															
Ala	Ser	Ala	Pro	Ile	Gly	Ser	Ala	Ile	Pro	Arg	Asn	Asn	Trp	Ala	Val
1				5					10					15	
Thr	Cys	Asp	Ser	Ala	Gln	Ser	Gly	Asn	Glu	Cys	Asn	Lys	Ala	Ile	Asp
			20					25					30		
Gly	Asn	Lys	Asp	Thr	Phe	Trp	His	Thr	Phe	Tyr	Gly	Ala	Asn	Gly	Asp
		35					40					45			
Pro	Lys	Pro	Pro	His	Thr	Tyr	Thr	Ile	Asp	Met	Lys	Thr	Thr	Gln	Asn
	50					55					60				
Val	Asn	Gly	Leu	Ser	Met	Leu	Pro	Arg	Gln	Asp	Gly	Asn	Gln	Asn	Gly
65					70					75				80	
Trp	Ile	Gly	Arg	His	Glu	Val	Tyr	Leu	Ser	Ser	Asp	Gly	Thr	Asn	Trp
				85					90					95	
Gly	Ser	Pro	Val	Ala	Ser	Gly	Ser	Trp	Phe	Ala	Asp	Ser	Thr	Thr	Lys
			100					105					110		
Tyr	Ser	Asn	Phe	Glu	Thr	Arg	Pro	Ala	Arg	Tyr	Val	Arg	Leu	Val	Ala
		115					120					125			
Ile	Thr	Glu	Ala	Asn	Gly	Gln	Pro	Trp	Thr	Ser	Ile	Ala	Glu	Ile	Asn
	130					135					140				
Val	Phe	Gln	Ala	Ser	Ser	Tyr	Thr	Ala	Pro	Gln	Pro	Gly	Leu	Gly	Arg
145					150					155					160
Trp	Gly	Pro	Thr	Ile	Asp	Leu	Pro	Ile	Val	Pro	Ala	Ala	Ala	Ala	Ile

				165				170					175			
Glu	Pro	Thr	Ser	Gly	Arg	Val	Leu	Met	Trp	Ser	Ser	Tyr	Arg	Asn	Asp	
			180					185					190			
Ala	Phe	Gly	Gly	Ser	Pro	Gly	Gly	Ile	Thr	Leu	Thr	Ser	Ser	Trp	Asp	
		195					200					205				
Pro	Ser	Thr	Gly	Ile	Val	Ser	Asp	Arg	Thr	Val	Thr	Val	Thr	Lys	His	
	210					215					220					
Asp	Met	Phe	Cys	Pro	Gly	Ile	Ser	Met	Asp	Gly	Asn	Gly	Gln	Ile	Val	
225					230					235					240	
Val	Thr	Gly	Gly	Asn	Asp	Ala	Lys	Lys	Thr	Ser	Leu	Tyr	Asp	Ser	Ser	
				245					250					255		
Ser	Asp	Ser	Trp	Ile	Pro	Gly	Pro	Asp	Met	Gln	Val	Ala	Arg	Gly	Tyr	
			260					265					270			
Gln	Ser	Ser	Ala	Thr	Met	Ser	Asp	Gly	Arg	Val	Phe	Thr	Ile	Gly	Gly	
		275					280					285				
Ser	Trp	Ser	Gly	Gly	Val	Phe	Glu	Lys	Asn	Gly	Glu	Val	Tyr	Ser	Pro	
	290					295				300						
Ser	Ser	Lys	Thr	Trp	Thr	Ser	Leu	Pro	Asn	Ala	Lys	Val	Asn	Pro	Met	
305					310					315					320	
Leu	Thr	Ala	Asp	Lys	Gln	Gly	Leu	Tyr	Arg	Ser	Asp	Asn	His	Ala	Trp	
				325					330					335		
Leu	Phe	Gly	Trp	Lys	Lys	Gly	Ser	Val	Phe	Gln	Ala	Gly	Pro	Ser	Thr	
		340					345					350				
Ala	Met	Asn	Trp	Tyr	Tyr	Thr	Ser	Gly	Ser	Gly	Asp	Val	Lys	Ser	Ala	
		355					360					365				
Gly	Lys	Arg	Gln	Ser	Asn	Arg	Gly	Val	Ala	Pro	Asp	Ala	Met	Cys	Gly	
	370				375						380					
Asn	Ala	Val	Met	Tyr	Asp	Ala	Val	Lys	Gly	Lys	Ile	Leu	Thr	Phe	Gly	
385					390					395					400	
Gly	Ser	Pro	Asp	Tyr	Gln	Asp	Ser	Asp	Ala	Thr	Thr	Asn	Ala	His	Ile	
				405				410						415		
Ile	Thr	Leu	Gly	Glu	Pro	Gly	Thr	Ser	Pro	Asn	Thr	Val	Phe	Ala	Ser	
			420				425					430				
Asn	Gly	Leu	Tyr	Phe	Ala	Arg	Thr	Phe	His	Thr	Ser	Val	Val	Leu	Pro	
		435					440					445				
Asp	Gly	Ser	Thr	Phe	Ile	Thr	Gly	Gly	Gln	Arg	Arg	Gly	Ile	Pro	Phe	
	450				455					460						
Glu	Asp	Ser	Thr	Pro	Val	Phe	Thr	Pro	Glu	Ile	Tyr	Val	Pro	Glu	Gln	
465					470					475					480	
Asp	Thr	Phe	Tyr	Lys	Gln	Asn	Pro	Asn	Ser	Ile	Val	Arg	Ala	Tyr	His	
				485				490						495		
Ser	Ile	Ser	Leu	Leu	Leu	Pro	Asp	Gly	Arg	Val	Phe	Asn	Gly	Gly	Gly	
			500					505					510			
Gly	Leu	Cys	Gly	Asp	Cys	Thr	Thr	Asn	His	Phe	Asp	Ala	Gln	Ile	Phe	
		515					520					525				
Thr	Pro	Asn	Tyr	Leu	Tyr	Asn	Ser	Asn	Gly	Asn	Leu	Ala	Thr	Arg	Pro	
	530					535					540					
Lys	Ile	Thr	Arg	Thr	Ser	Thr	Gln	Ser	Val	Lys	Val	Gly	Gly	Arg	Ile	
545					550					555					560	
Thr	Ile	Ser	Thr	Asp	Ser	Ser	Ile	Ser	Lys	Ala	Ser	Leu	Ile	Arg	Tyr	
				565				570						575		
Gly	Thr	Ala	Thr	His	Thr	Val	Asn	Thr	Asp	Gln	Arg	Arg	Ile	Pro	Leu	
			580					585					590			

Thr	Leu	Thr	Asn	Asn	Gly	Gly	Asn	Ser	Tyr	Ser	Phe	Gln	Val	Pro	Ser
		595					600					605			
Asp	Ser	Gly	Val	Ala	Leu	Pro	Gly	Tyr	Trp	Met	Leu	Phe	Val	Met	Asn
	610					615					620				
Ser	Ala	Gly	Val	Pro	Ser	Val	Ala	Ser	Thr	Ile	Arg	Val	Thr	Gln	
625					630					635					

<210> 14
 <211> 639
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Mutant 11.03.10C3 (A3, P136, G195E, V494A) of D.
 dendroides GaO

<400> 14															
Ala	Ser	Ala	Pro	Ile	Gly	Ser	Ala	Ile	Ser	Arg	Asn	Asn	Trp	Ala	Val
1				5					10					15	
Thr	Cys	Asp	Ser	Ala	Gln	Ser	Gly	Asn	Glu	Cys	Asn	Lys	Ala	Ile	Asp
			20					25					30		
Gly	Asn	Lys	Asp	Thr	Phe	Trp	His	Thr	Phe	Tyr	Gly	Ala	Asn	Gly	Asp
		35					40					45			
Pro	Lys	Pro	Pro	His	Thr	Tyr	Thr	Ile	Asp	Met	Lys	Thr	Thr	Gln	Asn
	50					55					60				
Val	Asn	Gly	Leu	Ser	Met	Leu	Pro	Arg	Gln	Asp	Gly	Asn	Gln	Asn	Gly
65					70					75				80	
Trp	Ile	Gly	Arg	His	Glu	Val	Tyr	Leu	Ser	Ser	Asp	Gly	Thr	Asn	Trp
				85					90					95	
Gly	Ser	Pro	Val	Ala	Ser	Gly	Ser	Trp	Phe	Ala	Asp	Ser	Thr	Thr	Lys
			100					105					110		
Tyr	Ser	Asn	Phe	Glu	Thr	Arg	Pro	Ala	Arg	Tyr	Val	Arg	Leu	Val	Ala
		115					120					125			
Ile	Thr	Glu	Ala	Asn	Gly	Gln	Pro	Trp	Thr	Ser	Ile	Ala	Glu	Ile	Asn
	130					135					140				
Val	Phe	Gln	Ala	Ser	Ser	Tyr	Thr	Ala	Pro	Gln	Pro	Gly	Leu	Gly	Arg
145					150					155					160
Trp	Gly	Pro	Thr	Ile	Asp	Leu	Pro	Ile	Val	Pro	Ala	Ala	Ala	Ala	Ile
				165					170					175	
Glu	Pro	Thr	Ser	Gly	Arg	Val	Leu	Met	Trp	Ser	Ser	Tyr	Arg	Asn	Asp
			180					185					190		
Ala	Phe	Glu	Gly	Ser	Pro	Gly	Gly	Ile	Thr	Leu	Thr	Ser	Ser	Trp	Asp
		195					200					205			
Pro	Ser	Thr	Gly	Ile	Val	Ser	Asp	Arg	Thr	Val	Thr	Val	Thr	Lys	His
	210					215						220			
Asp	Met	Phe	Cys	Pro	Gly	Ile	Ser	Met	Asp	Gly	Asn	Gly	Gln	Ile	Val
225					230					235					240
Val	Thr	Gly	Gly	Asn	Asp	Ala	Lys	Lys	Thr	Ser	Leu	Tyr	Asp	Ser	Ser
				245					250					255	
Ser	Asp	Ser	Trp	Ile	Pro	Gly	Pro	Asp	Met	Gln	Val	Ala	Arg	Gly	Tyr
			260					265					270		
Gln	Ser	Ser	Ala	Thr	Met	Ser	Asp	Gly	Arg	Val	Phe	Thr	Ile	Gly	Gly
		275					280						285		

Ser	Trp	Ser	Gly	Gly	Val	Phe	Glu	Lys	Asn	Gly	Glu	Val	Tyr	Ser	Pro
290						295					300				
Ser	Ser	Lys	Thr	Trp	Thr	Ser	Leu	Pro	Asn	Ala	Lys	Val	Asn	Pro	Met
305					310					315					320
Leu	Thr	Ala	Asp	Lys	Gln	Gly	Leu	Tyr	Arg	Ser	Asp	Asn	His	Ala	Trp
				325					330					335	
Leu	Phe	Gly	Trp	Lys	Lys	Gly	Ser	Val	Phe	Gln	Ala	Gly	Pro	Ser	Thr
			340					345					350		
Ala	Met	Asn	Trp	Tyr	Tyr	Thr	Ser	Gly	Ser	Gly	Asp	Val	Lys	Ser	Ala
		355					360					365			
Gly	Lys	Arg	Gln	Ser	Asn	Arg	Gly	Val	Ala	Pro	Asp	Ala	Met	Cys	Gly
	370					375					380				
Asn	Ala	Val	Met	Tyr	Asp	Ala	Val	Lys	Gly	Lys	Ile	Leu	Thr	Phe	Gly
385					390					395					400
Gly	Ser	Pro	Asp	Tyr	Gln	Asp	Ser	Asp	Ala	Thr	Thr	Asn	Ala	His	Ile
				405					410					415	
Ile	Thr	Leu	Gly	Glu	Pro	Gly	Thr	Ser	Pro	Asn	Thr	Val	Phe	Ala	Ser
			420					425					430		
Asn	Gly	Leu	Tyr	Phe	Ala	Arg	Thr	Phe	His	Thr	Ser	Val	Val	Leu	Pro
		435					440					445			
Asp	Gly	Ser	Thr	Phe	Ile	Thr	Gly	Gly	Gln	Arg	Arg	Gly	Ile	Pro	Phe
	450					455				460					
Glu	Asp	Ser	Thr	Pro	Val	Phe	Thr	Pro	Glu	Ile	Tyr	Val	Pro	Glu	Gln
465					470					475					480
Asp	Thr	Phe	Tyr	Lys	Gln	Asn	Pro	Asn	Ser	Ile	Val	Arg	Ala	Tyr	His
				485					490					495	
Ser	Ile	Ser	Leu	Leu	Leu	Pro	Asp	Gly	Arg	Val	Phe	Asn	Gly	Gly	Gly
			500					505					510		
Gly	Leu	Cys	Gly	Asp	Cys	Thr	Thr	Asn	His	Phe	Asp	Ala	Gln	Ile	Phe
		515					520					525			
Thr	Pro	Asn	Tyr	Leu	Tyr	Asn	Ser	Asn	Gly	Asn	Leu	Ala	Thr	Arg	Pro
	530					535					540				
Lys	Ile	Thr	Arg	Thr	Ser	Thr	Gln	Ser	Val	Lys	Val	Gly	Gly	Arg	Ile
545					550					555					560
Thr	Ile	Ser	Thr	Asp	Ser	Ser	Ile	Ser	Lys	Ala	Ser	Leu	Ile	Arg	Tyr
				565					570					575	
Gly	Thr	Ala	Thr	His	Thr	Val	Asn	Thr	Asp	Gln	Arg	Arg	Ile	Pro	Leu
			580					585					590		
Thr	Leu	Thr	Asn	Asn	Gly	Gly	Asn	Ser	Tyr	Ser	Phe	Gln	Val	Pro	Ser
		595					600					605			
Asp	Ser	Gly	Val	Ala	Leu	Pro	Gly	Tyr	Trp	Met	Leu	Phe	Val	Met	Asn
	610					615					620				
Ser	Ala	Gly	Val	Pro	Ser	Val	Ala	Ser	Thr	Ile	Arg	Val	Thr	Gln	
625					630					635					

<210> 15

<211> 639

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant 11.03.10D6 (P136, T218, L312, V494A, N535D)
of *D. dendroides* GaO

<400> 15

Ala	Ser	Ala	Pro	Ile	Gly	Ser	Ala	Ile	Ser	Arg	Asn	Asn	Trp	Ala	Val
1				5				10						15	
Thr	Cys	Asp	Ser	Ala	Gln	Ser	Gly	Asn	Glu	Cys	Asn	Lys	Ala	Ile	Asp
			20					25					30		
Gly	Asn	Lys	Asp	Thr	Phe	Trp	His	Thr	Phe	Tyr	Gly	Ala	Asn	Gly	Asp
		35					40					45			
Pro	Lys	Pro	Pro	His	Thr	Tyr	Thr	Ile	Asp	Met	Lys	Thr	Thr	Gln	Asn
	50					55					60				
Val	Asn	Gly	Leu	Ser	Met	Leu	Pro	Arg	Gln	Asp	Gly	Asn	Gln	Asn	Gly
65					70					75					80
Trp	Ile	Gly	Arg	His	Glu	Val	Tyr	Leu	Ser	Ser	Asp	Gly	Thr	Asn	Trp
				85					90					95	
Gly	Ser	Pro	Val	Ala	Ser	Gly	Ser	Trp	Phe	Ala	Asp	Ser	Thr	Thr	Lys
			100					105					110		
Tyr	Ser	Asn	Phe	Glu	Thr	Arg	Pro	Ala	Arg	Tyr	Val	Arg	Leu	Val	Ala
		115					120					125			
Ile	Thr	Glu	Ala	Asn	Gly	Gln	Pro	Trp	Thr	Ser	Ile	Ala	Glu	Ile	Asn
	130					135					140				
Val	Phe	Gln	Ala	Ser	Ser	Tyr	Thr	Ala	Pro	Gln	Pro	Gly	Leu	Gly	Arg
145					150					155					160
Trp	Gly	Pro	Thr	Ile	Asp	Leu	Pro	Ile	Val	Pro	Ala	Ala	Ala	Ala	Ile
				165					170					175	
Glu	Pro	Thr	Ser	Gly	Arg	Val	Leu	Met	Trp	Ser	Ser	Tyr	Arg	Asn	Asp
			180					185					190		
Ala	Phe	Gly	Gly	Ser	Pro	Gly	Gly	Ile	Thr	Leu	Thr	Ser	Ser	Trp	Asp
		195					200					205			
Pro	Ser	Thr	Gly	Ile	Val	Ser	Asp	Arg	Thr	Val	Thr	Val	Thr	Lys	His
		210				215					220				
Asp	Met	Phe	Cys	Pro	Gly	Ile	Ser	Met	Asp	Gly	Asn	Gly	Gln	Ile	Val
225					230					235					240
Val	Thr	Gly	Gly	Asn	Asp	Ala	Lys	Lys	Thr	Ser	Leu	Tyr	Asp	Ser	Ser
				245					250					255	
Ser	Asp	Ser	Trp	Ile	Pro	Gly	Pro	Asp	Met	Gln	Val	Ala	Arg	Gly	Tyr
			260					265					270		
Gln	Ser	Ser	Ala	Thr	Met	Ser	Asp	Gly	Arg	Val	Phe	Thr	Ile	Gly	Gly
		275					280					285			
Ser	Trp	Ser	Gly	Gly	Val	Phe	Glu	Lys	Asn	Gly	Glu	Val	Tyr	Ser	Pro
	290					295					300				
Ser	Ser	Lys	Thr	Trp	Thr	Ser	Leu	Pro	Asn	Ala	Lys	Val	Asn	Pro	Met
305					310					315					320
Leu	Thr	Ala	Asp	Lys	Gln	Gly	Leu	Tyr	Arg	Ser	Asp	Asn	His	Ala	Trp
				325					330					335	
Leu	Phe	Gly	Trp	Lys	Lys	Gly	Ser	Val	Phe	Gln	Ala	Gly	Pro	Ser	Thr
			340					345					350		
Ala	Met	Asn	Trp	Tyr	Tyr	Thr	Ser	Gly	Ser	Gly	Asp	Val	Lys	Ser	Ala
		355					360					365			
Gly	Lys	Arg	Gln	Ser	Asn	Arg	Gly	Val	Ala	Pro	Asp	Ala	Met	Cys	Gly
	370					375					380				
Asn	Ala	Val	Met	Tyr	Asp	Ala	Val	Lys	Gly	Lys	Ile	Leu	Thr	Phe	Gly
385					390					395					400
Gly	Ser	Pro	Asp	Tyr	Gln	Asp	Ser	Asp	Ala	Thr	Thr	Asn	Ala	His	Ile

				405					410					415			
Ile	Thr	Leu	Gly	Glu	Pro	Gly	Thr	Ser	Pro	Asn	Thr	Val	Phe	Ala	Ser		
			420					425					430				
Asn	Gly	Leu	Tyr	Phe	Ala	Arg	Thr	Phe	His	Thr	Ser	Val	Val	Leu	Pro		
		435					440					445					
Asp	Gly	Ser	Thr	Phe	Ile	Thr	Gly	Gly	Gln	Arg	Arg	Gly	Ile	Pro	Phe		
	450					455					460						
Glu	Asp	Ser	Thr	Pro	Val	Phe	Thr	Pro	Glu	Ile	Tyr	Val	Pro	Glu	Gln		
465					470					475					480		
Asp	Thr	Phe	Tyr	Lys	Gln	Asn	Pro	Asn	Ser	Ile	Val	Arg	Ala	Tyr	His		
				485				490						495			
Ser	Ile	Ser	Leu	Leu	Pro	Asp	Gly	Arg	Val	Phe	Asn	Gly	Gly	Gly			
		500					505					510					
Gly	Leu	Cys	Gly	Asp	Cys	Thr	Thr	Asn	His	Phe	Asp	Ala	Gln	Ile	Phe		
	515					520					525						
Thr	Pro	Asn	Tyr	Leu	Tyr	Asp	Ser	Asn	Gly	Asn	Leu	Ala	Thr	Arg	Pro		
	530				535						540						
Lys	Ile	Thr	Arg	Thr	Ser	Thr	Gln	Ser	Val	Lys	Val	Gly	Gly	Arg	Ile		
545					550				555						560		
Thr	Ile	Ser	Thr	Asp	Ser	Ser	Ile	Ser	Lys	Ala	Ser	Leu	Ile	Arg	Tyr		
				565				570						575			
Gly	Thr	Ala	Thr	His	Thr	Val	Asn	Thr	Asp	Gln	Arg	Arg	Ile	Pro	Leu		
			580				585					590					
Thr	Leu	Thr	Asn	Asn	Gly	Gly	Asn	Ser	Tyr	Ser	Phe	Gln	Val	Pro	Ser		
	595				600						605						
Asp	Ser	Gly	Val	Ala	Leu	Pro	Gly	Tyr	Trp	Met	Leu	Phe	Val	Met	Asn		
	610				615					620							
Ser	Ala	Gly	Val	Pro	Ser	Val	Ala	Ser	Thr	Ile	Arg	Val	Thr	Gln			
625					630					635							

<210> 16
 <211> 639
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Mutant 11.03.13E12 (M70V, P136, V494A) from D.
 Dendroides GaO

				<400>													
Ala	Ser	Ala	Pro	Ile	Gly	Ser	Ala	Ile	Ser	Arg	Asn	Asn	Trp	Ala	Val		
1				5				10					15				
Thr	Cys	Asp	Ser	Ala	Gln	Ser	Gly	Asn	Glu	Cys	Asn	Lys	Ala	Ile	Asp		
		20					25					30					
Gly	Asn	Lys	Asp	Thr	Phe	Trp	His	Thr	Phe	Tyr	Gly	Ala	Asn	Gly	Asp		
	35					40					45						
Pro	Lys	Pro	Pro	His	Thr	Tyr	Thr	Ile	Asp	Met	Lys	Thr	Thr	Gln	Asn		
	50				55				60								
Val	Asn	Gly	Leu	Ser	Val	Leu	Pro	Arg	Gln	Asp	Gly	Asn	Gln	Asn	Gly		
65					70				75					80			
Trp	Ile	Gly	Arg	His	Glu	Val	Tyr	Leu	Ser	Ser	Asp	Gly	Thr	Asn	Trp		
				85				90						95			
Gly	Ser	Pro	Val	Ala	Ser	Gly	Ser	Trp	Phe	Ala	Asp	Ser	Thr	Thr	Lys		

			100					105				110					
Tyr	Ser	Asn	Phe	Glu	Thr	Arg	Pro	Ala	Arg	Tyr	Val	Arg	Leu	Val	Ala		
		115					120					125					
Ile	Thr	Glu	Ala	Asn	Gly	Gln	Pro	Trp	Thr	Ser	Ile	Ala	Glu	Ile	Asn		
	130					135					140						
Val	Phe	Gln	Ala	Ser	Ser	Tyr	Thr	Ala	Pro	Gln	Pro	Gly	Leu	Gly	Arg		
145				150						155					160		
Trp	Gly	Pro	Thr	Ile	Asp	Leu	Pro	Ile	Val	Pro	Ala	Ala	Ala	Ala	Ile		
			165						170					175			
Glu	Pro	Thr	Ser	Gly	Arg	Val	Leu	Met	Trp	Ser	Ser	Tyr	Arg	Asn	Asp		
		180						185					190				
Ala	Phe	Gly	Gly	Ser	Pro	Gly	Gly	Ile	Thr	Leu	Thr	Ser	Ser	Trp	Asp		
	195						200					205					
Pro	Ser	Thr	Gly	Ile	Val	Ser	Asp	Arg	Thr	Val	Thr	Val	Thr	Lys	His		
	210					215					220						
Asp	Met	Phe	Cys	Pro	Gly	Ile	Ser	Met	Asp	Gly	Asn	Gly	Gln	Ile	Val		
225				230						235					240		
Val	Thr	Gly	Gly	Asn	Asp	Ala	Lys	Lys	Thr	Ser	Leu	Tyr	Asp	Ser	Ser		
			245						250					255			
Ser	Asp	Ser	Trp	Ile	Pro	Gly	Pro	Asp	Met	Gln	Val	Ala	Arg	Gly	Tyr		
		260						265					270				
Gln	Ser	Ser	Ala	Thr	Met	Ser	Asp	Gly	Arg	Val	Phe	Thr	Ile	Gly	Gly		
	275					280						285					
Ser	Trp	Ser	Gly	Gly	Val	Phe	Glu	Lys	Asn	Gly	Glu	Val	Tyr	Ser	Pro		
	290				295						300						
Ser	Ser	Lys	Thr	Trp	Thr	Ser	Leu	Pro	Asn	Ala	Lys	Val	Asn	Pro	Met		
305				310						315					320		
Leu	Thr	Ala	Asp	Lys	Gln	Gly	Leu	Tyr	Arg	Ser	Asp	Asn	His	Ala	Trp		
			325						330					335			
Leu	Phe	Gly	Trp	Lys	Lys	Gly	Ser	Val	Phe	Gln	Ala	Gly	Pro	Ser	Thr		
		340						345					350				
Ala	Met	Asn	Trp	Tyr	Tyr	Thr	Ser	Gly	Ser	Gly	Asp	Val	Lys	Ser	Ala		
	355						360					365					
Gly	Lys	Arg	Gln	Ser	Asn	Arg	Gly	Val	Ala	Pro	Asp	Ala	Met	Cys	Gly		
	370				375						380						
Asn	Ala	Val	Met	Tyr	Asp	Ala	Val	Lys	Gly	Lys	Ile	Leu	Thr	Phe	Gly		
385				390						395					400		
Gly	Ser	Pro	Asp	Tyr	Gln	Asp	Ser	Asp	Ala	Thr	Thr	Asn	Ala	His	Ile		
			405						410					415			
Ile	Thr	Leu	Gly	Glu	Pro	Gly	Thr	Ser	Pro	Asn	Thr	Val	Phe	Ala	Ser		
		420						425					430				
Asn	Gly	Leu	Tyr	Phe	Ala	Arg	Thr	Phe	His	Thr	Ser	Val	Val	Leu	Pro		
	435						440					445					
Asp	Gly	Ser	Thr	Phe	Ile	Thr	Gly	Gly	Gln	Arg	Arg	Gly	Ile	Pro	Phe		
	450					455					460						
Glu	Asp	Ser	Thr	Pro	Val	Phe	Thr	Pro	Glu	Ile	Tyr	Val	Pro	Glu	Gln		
465				470						475					480		
Asp	Thr	Phe	Tyr	Lys	Gln	Asn	Pro	Asn	Ser	Ile	Val	Arg	Ala	Tyr	His		
			485					490						495			
Ser	Ile	Ser	Leu	Leu	Leu	Pro	Asp	Gly	Arg	Val	Phe	Asn	Gly	Gly	Gly		
		500						505					510				
Gly	Leu	Cys	Gly	Asp	Cys	Thr	Thr	Asn	His	Phe	Asp	Ala	Gln	Ile	Phe		
		515					520					525					

Thr	Pro	Asn	Tyr	Leu	Tyr	Asn	Ser	Asn	Gly	Asn	Leu	Ala	Thr	Arg	Pro
	530					535					540				
Lys	Ile	Thr	Arg	Thr	Ser	Thr	Gln	Ser	Val	Lys	Val	Gly	Gly	Arg	Ile
545					550					555					560
Thr	Ile	Ser	Thr	Asp	Ser	Ser	Ile	Ser	Lys	Ala	Ser	Leu	Ile	Arg	Tyr
				565					570					575	
Gly	Thr	Ala	Thr	His	Thr	Val	Asn	Thr	Asp	Gln	Arg	Arg	Ile	Pro	Leu
			580					585					590		
Thr	Leu	Thr	Asn	Asn	Gly	Gly	Asn	Ser	Tyr	Ser	Phe	Gln	Val	Pro	Ser
		595					600					605			
Asp	Ser	Gly	Val	Ala	Leu	Pro	Gly	Tyr	Trp	Met	Leu	Phe	Val	Met	Asn
610						615					620				
Ser	Ala	Gly	Val	Pro	Ser	Val	Ala	Ser	Thr	Ile	Arg	Val	Thr	Gln	
625					630					635					

<210> 17

<211> 639

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant 1.06.20E7 (S10P, M70V, P136, G195E, V494A, N535D) from D. Dendroides GaO

<400> 17

Ala	Ser	Ala	Pro	Ile	Gly	Ser	Ala	Ile	Pro	Arg	Asn	Asn	Trp	Ala	Val
1				5					10					15	
Thr	Cys	Asp	Ser	Ala	Gln	Ser	Gly	Asn	Glu	Cys	Asn	Lys	Ala	Ile	Asp
		20					25					30			
Gly	Asn	Lys	Asp	Thr	Phe	Trp	His	Thr	Phe	Tyr	Gly	Ala	Asn	Gly	Asp
	35					40					45				
Pro	Lys	Pro	Pro	His	Thr	Tyr	Thr	Ile	Asp	Met	Lys	Thr	Thr	Gln	Asn
50					55						60				
Val	Asn	Gly	Leu	Ser	Val	Leu	Pro	Arg	Gln	Asp	Gly	Asn	Gln	Asn	Gly
65					70				75					80	
Trp	Ile	Gly	Arg	His	Glu	Val	Tyr	Leu	Ser	Ser	Asp	Gly	Thr	Asn	Trp
			85				90						95		
Gly	Ser	Pro	Val	Ala	Ser	Gly	Ser	Trp	Phe	Ala	Asp	Ser	Thr	Thr	Lys
		100					105						110		
Tyr	Ser	Asn	Phe	Glu	Thr	Arg	Pro	Ala	Arg	Tyr	Val	Arg	Leu	Val	Ala
	115					120						125			
Ile	Thr	Glu	Ala	Asn	Gly	Gln	Pro	Trp	Thr	Ser	Ile	Ala	Glu	Ile	Asn
130					135						140				
Val	Phe	Gln	Ala	Ser	Ser	Tyr	Thr	Ala	Pro	Gln	Pro	Gly	Leu	Gly	Arg
145					150					155					160
Trp	Gly	Pro	Thr	Ile	Asp	Leu	Pro	Ile	Val	Pro	Ala	Ala	Ala	Ala	Ile
			165						170					175	
Glu	Pro	Thr	Ser	Gly	Arg	Val	Leu	Met	Trp	Ser	Ser	Tyr	Arg	Asn	Asp
		180					185						190		
Ala	Phe	Glu	Gly	Ser	Pro	Gly	Gly	Ile	Thr	Leu	Thr	Ser	Ser	Trp	Asp
	195					200						205			
Pro	Ser	Thr	Gly	Ile	Val	Ser	Asp	Arg	Thr	Val	Thr	Val	Thr	Lys	His
210						215						220			

Asp	Met	Phe	Cys	Pro	Gly	Ile	Ser	Met	Asp	Gly	Asn	Gly	Gln	Ile	Val
225					230					235					240
Val	Thr	Gly	Gly	Asn	Asp	Ala	Lys	Lys	Thr	Ser	Leu	Tyr	Asp	Ser	Ser
				245					250					255	
Ser	Asp	Ser	Trp	Ile	Pro	Gly	Pro	Asp	Met	Gln	Val	Ala	Arg	Gly	Tyr
			260					265					270		
Gln	Ser	Ser	Ala	Thr	Met	Ser	Asp	Gly	Arg	Val	Phe	Thr	Ile	Gly	Gly
		275					280					285			
Ser	Trp	Ser	Gly	Gly	Val	Phe	Glu	Lys	Asn	Gly	Glu	Val	Tyr	Ser	Pro
	290					295					300				
Ser	Ser	Lys	Thr	Trp	Thr	Ser	Leu	Pro	Asn	Ala	Lys	Val	Asn	Pro	Met
305					310					315					320
Leu	Thr	Ala	Asp	Lys	Gln	Gly	Leu	Tyr	Arg	Ser	Asp	Asn	His	Ala	Trp
				325					330					335	
Leu	Phe	Gly	Trp	Lys	Lys	Gly	Ser	Val	Phe	Gln	Ala	Gly	Pro	Ser	Thr
			340					345					350		
Ala	Met	Asn	Trp	Tyr	Tyr	Thr	Ser	Gly	Ser	Gly	Asp	Val	Lys	Ser	Ala
		355					360					365			
Gly	Lys	Arg	Gln	Ser	Asn	Arg	Gly	Val	Ala	Pro	Asp	Ala	Met	Cys	Gly
	370					375					380				
Asn	Ala	Val	Met	Tyr	Asp	Ala	Val	Lys	Gly	Lys	Ile	Leu	Thr	Phe	Gly
385					390					395					400
Gly	Ser	Pro	Asp	Tyr	Gln	Asp	Ser	Asp	Ala	Thr	Thr	Asn	Ala	His	Ile
				405					410					415	
Ile	Thr	Leu	Gly	Glu	Pro	Gly	Thr	Ser	Pro	Asn	Thr	Val	Phe	Ala	Ser
			420					425					430		
Asn	Gly	Leu	Tyr	Phe	Ala	Arg	Thr	Phe	His	Thr	Ser	Val	Val	Leu	Pro
		435					440					445			
Asp	Gly	Ser	Thr	Phe	Ile	Thr	Gly	Gly	Gln	Arg	Arg	Gly	Ile	Pro	Phe
	450					455					460				
Glu	Asp	Ser	Thr	Pro	Val	Phe	Thr	Pro	Glu	Ile	Tyr	Val	Pro	Glu	Gln
465					470					475					480
Asp	Thr	Phe	Tyr	Lys	Gln	Asn	Pro	Asn	Ser	Ile	Val	Arg	Ala	Tyr	His
				485					490					495	
Ser	Ile	Ser	Leu	Leu	Pro	Asp	Gly	Arg	Val	Phe	Asn	Gly	Gly	Gly	
			500				505					510			
Gly	Leu	Cys	Gly	Asp	Cys	Thr	Thr	Asn	His	Phe	Asp	Ala	Gln	Ile	Phe
		515					520					525			
Thr	Pro	Asn	Tyr	Leu	Tyr	Asp	Ser	Asn	Gly	Asn	Leu	Ala	Thr	Arg	Pro
	530					535					540				
Lys	Ile	Thr	Arg	Thr	Ser	Thr	Gln	Ser	Val	Lys	Val	Gly	Gly	Arg	Ile
545					550					555					560
Thr	Ile	Ser	Thr	Asp	Ser	Ser	Ile	Ser	Lys	Ala	Ser	Leu	Ile	Arg	Tyr
				565					570					575	
Gly	Thr	Ala	Thr	His	Thr	Val	Asn	Thr	Asp	Gln	Arg	Arg	Ile	Pro	Leu
			580					585					590		
Thr	Leu	Thr	Asn	Asn	Gly	Gly	Asn	Ser	Tyr	Ser	Phe	Gln	Val	Pro	Ser
		595					600					605			
Asp	Ser	Gly	Val	Ala	Leu	Pro	Gly	Tyr	Trp	Met	Leu	Phe	Val	Met	Asn
	610					615					620				
Ser	Ala	Gly	Val	Pro	Ser	Val	Ala	Ser	Thr	Ile	Arg	Val	Thr	Gln	
625					630					635					

<210> 18
 <211> 639
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Mutant 1.D4 (N413D) from D. Dendroides GaO

<400> 18

Ala	Ser	Ala	Pro	Ile	Gly	Ser	Ala	Ile	Ser	Arg	Asn	Asn	Trp	Ala	Val
1				5					10					15	
Thr	Cys	Asp	Ser	Ala	Gln	Ser	Gly	Asn	Glu	Cys	Asn	Lys	Ala	Ile	Asp
			20					25					30		
Gly	Asn	Lys	Asp	Thr	Phe	Trp	His	Thr	Phe	Tyr	Gly	Ala	Asn	Gly	Asp
	35						40					45			
Pro	Lys	Pro	Pro	His	Thr	Tyr	Thr	Ile	Asp	Met	Lys	Thr	Thr	Gln	Asn
	50					55					60				
Val	Asn	Gly	Leu	Ser	Met	Leu	Pro	Arg	Gln	Asp	Gly	Asn	Gln	Asn	Gly
65					70					75					80
Trp	Ile	Gly	Arg	His	Glu	Val	Tyr	Leu	Ser	Ser	Asp	Gly	Thr	Asn	Trp
				85					90					95	
Gly	Ser	Pro	Val	Ala	Ser	Gly	Ser	Trp	Phe	Ala	Asp	Ser	Thr	Thr	Lys
			100					105					110		
Tyr	Ser	Asn	Phe	Glu	Thr	Arg	Pro	Ala	Arg	Tyr	Val	Arg	Leu	Val	Ala
		115					120					125			
Ile	Thr	Glu	Ala	Asn	Gly	Gln	Pro	Trp	Thr	Ser	Ile	Ala	Glu	Ile	Asn
	130					135					140				
Val	Phe	Gln	Ala	Ser	Ser	Tyr	Thr	Ala	Pro	Gln	Pro	Gly	Leu	Gly	Arg
145					150					155					160
Trp	Gly	Pro	Thr	Ile	Asp	Leu	Pro	Ile	Val	Pro	Ala	Ala	Ala	Ala	Ile
				165					170					175	
Glu	Pro	Thr	Ser	Gly	Arg	Val	Leu	Met	Trp	Ser	Ser	Tyr	Arg	Asn	Asp
			180					185					190		
Ala	Phe	Gly	Gly	Ser	Pro	Gly	Gly	Ile	Thr	Leu	Thr	Ser	Ser	Trp	Asp
		195					200					205			
Pro	Ser	Thr	Gly	Ile	Val	Ser	Asp	Arg	Thr	Val	Thr	Val	Thr	Lys	His
	210					215					220				
Asp	Met	Phe	Cys	Pro	Gly	Ile	Ser	Met	Asp	Gly	Asn	Gly	Gln	Ile	Val
225					230					235					240
Val	Thr	Gly	Gly	Asn	Asp	Ala	Lys	Lys	Thr	Ser	Leu	Tyr	Asp	Ser	Ser
				245					250					255	
Ser	Asp	Ser	Trp	Ile	Pro	Gly	Pro	Asp	Met	Gln	Val	Ala	Arg	Gly	Tyr
			260					265					270		
Gln	Ser	Ser	Ala	Thr	Met	Ser	Asp	Gly	Arg	Val	Phe	Thr	Ile	Gly	Gly
		275					280					285			
Ser	Trp	Ser	Gly	Gly	Val	Phe	Glu	Lys	Asn	Gly	Glu	Val	Tyr	Ser	Pro
	290					295					300				
Ser	Ser	Lys	Thr	Trp	Thr	Ser	Leu	Pro	Asn	Ala	Lys	Val	Asn	Pro	Met
305					310					315					320
Leu	Thr	Ala	Asp	Lys	Gln	Gly	Leu	Tyr	Arg	Ser	Asp	Asn	His	Ala	Trp
				325					330					335	
Leu	Phe	Gly	Trp	Lys	Lys	Gly	Ser	Val	Phe	Gln	Ala	Gly	Pro	Ser	Thr
			340					345					350		

Ala	Met	Asn	Trp	Tyr	Tyr	Thr	Ser	Gly	Ser	Gly	Asp	Val	Lys	Ser	Ala
		355					360					365			
Gly	Lys	Arg	Gln	Ser	Asn	Arg	Gly	Val	Ala	Pro	Asp	Ala	Met	Cys	Gly
	370					375					380				
Asn	Ala	Val	Met	Tyr	Asp	Ala	Val	Lys	Gly	Lys	Ile	Leu	Thr	Phe	Gly
385					390					395					400
Gly	Ser	Pro	Asp	Tyr	Gln	Asp	Ser	Asp	Ala	Thr	Thr	Asp	Ala	His	Ile
			405					410						415	
Ile	Thr	Leu	Gly	Glu	Pro	Gly	Thr	Ser	Pro	Asn	Thr	Val	Phe	Ala	Ser
			420					425					430		
Asn	Gly	Leu	Tyr	Phe	Ala	Arg	Thr	Phe	His	Thr	Ser	Val	Val	Leu	Pro
		435					440					445			
Asp	Gly	Ser	Thr	Phe	Ile	Thr	Gly	Gly	Gln	Arg	Arg	Gly	Ile	Pro	Phe
	450					455					460				
Glu	Asp	Ser	Thr	Pro	Val	Phe	Thr	Pro	Glu	Ile	Tyr	Val	Pro	Glu	Gln
465					470					475					480
Asp	Thr	Phe	Tyr	Lys	Gln	Asn	Pro	Asn	Ser	Ile	Val	Arg	Val	Tyr	His
			485						490					495	
Ser	Ile	Ser	Leu	Leu	Leu	Pro	Asp	Gly	Arg	Val	Phe	Asn	Gly	Gly	Gly
			500					505					510		
Gly	Leu	Cys	Gly	Asp	Cys	Thr	Thr	Asn	His	Phe	Asp	Ala	Gln	Ile	Phe
		515					520					525			
Thr	Pro	Asn	Tyr	Leu	Tyr	Asn	Ser	Asn	Gly	Asn	Leu	Ala	Thr	Arg	Pro
	530					535					540				
Lys	Ile	Thr	Arg	Thr	Ser	Thr	Gln	Ser	Val	Lys	Val	Gly	Gly	Arg	Ile
545					550					555					560
Thr	Ile	Ser	Thr	Asp	Ser	Ser	Ile	Ser	Lys	Ala	Ser	Leu	Ile	Arg	Tyr
			565						570					575	
Gly	Thr	Ala	Thr	His	Thr	Val	Asn	Thr	Asp	Gln	Arg	Arg	Ile	Pro	Leu
			580					585					590		
Thr	Leu	Thr	Asn	Asn	Gly	Gly	Asn	Ser	Tyr	Ser	Phe	Gln	Val	Pro	Ser
		595					600					605			
Asp	Ser	Gly	Val	Ala	Leu	Pro	Gly	Tyr	Trp	Met	Leu	Phe	Val	Met	Asn
	610					615					620				
Ser	Ala	Gly	Val	Pro	Ser	Val	Ala	Ser	Thr	Ile	Arg	Val	Thr	Gln	
625					630					635					

<210> 19

<211> 639

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant 2.G4 (N413D, S550) from D. Dendroides GaO

<400> 19

Ala	Ser	Ala	Pro	Ile	Gly	Ser	Ala	Ile	Ser	Arg	Asn	Asn	Trp	Ala	Val
1				5				10					15		
Thr	Cys	Asp	Ser	Ala	Gln	Ser	Gly	Asn	Glu	Cys	Asn	Lys	Ala	Ile	Asp
			20					25				30			
Gly	Asn	Lys	Asp	Thr	Phe	Trp	His	Thr	Phe	Tyr	Gly	Ala	Asn	Gly	Asp
		35					40					45			
Pro	Lys	Pro	Pro	His	Thr	Tyr	Thr	Ile	Asp	Met	Lys	Thr	Thr	Gln	Asn

50	55	60
Val Asn Gly Leu Ser Met	Leu Pro Arg Gln Asp	Gly Asn Gln Asn Gly
65	70	75
Trp Ile Gly Arg His Glu	Val Tyr Leu Ser Ser	Asp Gly Thr Asn Trp
	85	90
Gly Ser Pro Val Ala Ser	Gly Ser Trp Phe Ala	Asp Ser Thr Thr Lys
	100	105
Tyr Ser Asn Phe Glu Thr	Arg Pro Ala Arg Tyr	Val Arg Leu Val Ala
	115	120
Ile Thr Glu Ala Asn Gly	Gln Pro Trp Thr Ser	Ile Ala Glu Ile Asn
	130	135
Val Phe Gln Ala Ser Ser	Tyr Thr Ala Pro Gln	Pro Gly Leu Gly Arg
145	150	155
Trp Gly Pro Thr Ile Asp	Leu Pro Ile Val Pro	Ala Ala Ala Ala Ile
	165	170
Glu Pro Thr Ser Gly Arg	Val Leu Met Trp Ser	Ser Ser Tyr Arg Asn Asp
	180	185
Ala Phe Gly Gly Ser Pro	Gly Gly Ile Thr Leu	Thr Ser Ser Trp Asp
	195	200
Pro Ser Thr Gly Ile Val	Ser Asp Arg Thr Val	Thr Val Thr Lys His
	210	215
Asp Met Phe Cys Pro Gly	Ile Ser Met Asp Gly	Asn Gly Gln Ile Val
225	230	235
Val Thr Gly Gly Asn Asp	Ala Lys Lys Thr Ser	Leu Tyr Asp Ser Ser
	245	250
Ser Asp Ser Trp Ile Pro	Gly Pro Asp Met Gln	Val Ala Arg Gly Tyr
	260	265
Gln Ser Ser Ala Thr Met	Ser Asp Gly Arg Val	Phe Thr Ile Gly Gly
	275	280
Ser Trp Ser Gly Gly Val	Phe Glu Lys Asn Gly	Glu Val Tyr Ser Pro
	295	300
Ser Ser Lys Thr Trp Thr	Ser Leu Pro Asn Ala	Lys Val Asn Pro Met
305	310	315
Leu Thr Ala Asp Lys Gln	Gly Leu Tyr Arg Ser	Asp Asn His Ala Trp
	325	330
Leu Phe Gly Trp Lys Lys	Gly Ser Val Phe Gln	Ala Gly Pro Ser Thr
	340	345
Ala Met Asn Trp Tyr Tyr	Thr Ser Gly Ser Gly	Asp Val Lys Ser Ala
	355	360
Gly Lys Arg Gln Ser Asn	Arg Gly Val Ala Pro	Asp Ala Met Cys Gly
	375	380
Asn Ala Val Met Tyr Asp	Ala Val Lys Gly Lys	Ile Leu Thr Phe Gly
385	390	395
Gly Ser Pro Asp Tyr Gln	Asp Ser Asp Ala Thr	Thr Thr Asp Ala His
	405	410
Ile Thr Leu Gly Glu Pro	Gly Thr Ser Pro Asn	Thr Val Phe Ala Ser
	420	425
Asn Gly Leu Tyr Phe Ala	Arg Thr Phe His Thr	Ser Val Val Leu Pro
	435	440
Asp Gly Ser Thr Phe Ile	Thr Gly Gly Gln Arg	Arg Gly Ile Pro Phe
	455	460
Glu Asp Ser Thr Pro Val	Phe Thr Pro Glu Ile	Tyr Val Pro Glu Gln
465	470	475
		480

Asp	Thr	Phe	Tyr	Lys	Gln	Asn	Pro	Asn	Ser	Ile	Val	Arg	Val	Tyr	His
				485					490					495	
Ser	Ile	Ser	Leu	Leu	Leu	Pro	Asp	Gly	Arg	Val	Phe	Asn	Gly	Gly	Gly
			500					505					510		
Gly	Leu	Cys	Gly	Asp	Cys	Thr	Thr	Asn	His	Phe	Asp	Ala	Gln	Ile	Phe
		515					520					525			
Thr	Pro	Asn	Tyr	Leu	Tyr	Asn	Ser	Asn	Gly	Asn	Leu	Ala	Thr	Arg	Pro
	530					535					540				
Lys	Ile	Thr	Arg	Thr	Ser	Thr	Gln	Ser	Val	Lys	Val	Gly	Gly	Arg	Ile
545					550					555					560
Thr	Ile	Ser	Thr	Asp	Ser	Ser	Ile	Ser	Lys	Ala	Ser	Leu	Ile	Arg	Tyr
				565					570					575	
Gly	Thr	Ala	Thr	His	Thr	Val	Asn	Thr	Asp	Gln	Arg	Arg	Ile	Pro	Leu
			580					585					590		
Thr	Leu	Thr	Asn	Asn	Gly	Gly	Asn	Ser	Tyr	Ser	Phe	Gln	Val	Pro	Ser
		595					600					605			
Asp	Ser	Gly	Val	Ala	Leu	Pro	Gly	Tyr	Trp	Met	Leu	Phe	Val	Met	Asn
	610					615					620				
Ser	Ala	Gly	Val	Pro	Ser	Val	Ala	Ser	Thr	Ile	Arg	Val	Thr	Gln	
625					630					635					

<210> 20
 <211> 639
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Mutant 3.H7 (N413D, S550, V494A) from D.
 Dendroides GaO

<400> 20															
Ala	Ser	Ala	Pro	Ile	Gly	Ser	Ala	Ile	Ser	Arg	Asn	Asn	Trp	Ala	Val
1				5					10				15		
Thr	Cys	Asp	Ser	Ala	Gln	Ser	Gly	Asn	Glu	Cys	Asn	Lys	Ala	Ile	Asp
			20					25				30			
Gly	Asn	Lys	Asp	Thr	Phe	Trp	His	Thr	Phe	Tyr	Gly	Ala	Asn	Gly	Asp
		35					40					45			
Pro	Lys	Pro	Pro	His	Thr	Tyr	Thr	Ile	Asp	Met	Lys	Thr	Thr	Gln	Asn
	50					55					60				
Val	Asn	Gly	Leu	Ser	Met	Leu	Pro	Arg	Gln	Asp	Gly	Asn	Gln	Asn	Gly
65					70					75					80
Trp	Ile	Gly	Arg	His	Glu	Val	Tyr	Leu	Ser	Ser	Asp	Gly	Thr	Asn	Trp
				85					90					95	
Gly	Ser	Pro	Val	Ala	Ser	Gly	Ser	Trp	Phe	Ala	Asp	Ser	Thr	Thr	Lys
			100					105					110		
Tyr	Ser	Asn	Phe	Glu	Thr	Arg	Pro	Ala	Arg	Tyr	Val	Arg	Leu	Val	Ala
		115					120					125			
Ile	Thr	Glu	Ala	Asn	Gly	Gln	Pro	Trp	Thr	Ser	Ile	Ala	Glu	Ile	Asn
	130					135					140				
Val	Phe	Gln	Ala	Ser	Ser	Tyr	Thr	Ala	Pro	Gln	Pro	Gly	Leu	Gly	Arg
145					150					155					160
Trp	Gly	Pro	Thr	Ile	Asp	Leu	Pro	Ile	Val	Pro	Ala	Ala	Ala	Ala	Ile
				165					170					175	

Glu	Pro	Thr	Ser	Gly	Arg	Val	Leu	Met	Trp	Ser	Ser	Tyr	Arg	Asn	Asp
			180					185					190		
Ala	Phe	Gly	Gly	Ser	Pro	Gly	Gly	Ile	Thr	Leu	Thr	Ser	Ser	Trp	Asp
		195					200					205			
Pro	Ser	Thr	Gly	Ile	Val	Ser	Asp	Arg	Thr	Val	Thr	Val	Thr	Lys	His
	210					215					220				
Asp	Met	Phe	Cys	Pro	Gly	Ile	Ser	Met	Asp	Gly	Asn	Gly	Gln	Ile	Val
225					230					235					240
Val	Thr	Gly	Gly	Asn	Asp	Ala	Lys	Lys	Thr	Ser	Leu	Tyr	Asp	Ser	Ser
				245					250					255	
Ser	Asp	Ser	Trp	Ile	Pro	Gly	Pro	Asp	Met	Gln	Val	Ala	Arg	Gly	Tyr
			260					265					270		
Gln	Ser	Ser	Ala	Thr	Met	Ser	Asp	Gly	Arg	Val	Phe	Thr	Ile	Gly	Gly
		275					280					285			
Ser	Trp	Ser	Gly	Gly	Val	Phe	Glu	Lys	Asn	Gly	Glu	Val	Tyr	Ser	Pro
	290					295					300				
Ser	Ser	Lys	Thr	Trp	Thr	Ser	Leu	Pro	Asn	Ala	Lys	Val	Asn	Pro	Met
305					310					315					320
Leu	Thr	Ala	Asp	Lys	Gln	Gly	Leu	Tyr	Arg	Ser	Asp	Asn	His	Ala	Trp
				325					330					335	
Leu	Phe	Gly	Trp	Lys	Lys	Gly	Ser	Val	Phe	Gln	Ala	Gly	Pro	Ser	Thr
			340					345					350		
Ala	Met	Asn	Trp	Tyr	Tyr	Thr	Ser	Gly	Ser	Gly	Asp	Val	Lys	Ser	Ala
		355					360					365			
Gly	Lys	Arg	Gln	Ser	Asn	Arg	Gly	Val	Ala	Pro	Asp	Ala	Met	Cys	Gly
	370					375					380				
Asn	Ala	Val	Met	Tyr	Asp	Ala	Val	Lys	Gly	Lys	Ile	Leu	Thr	Phe	Gly
385					390					395					400
Gly	Ser	Pro	Asp	Tyr	Gln	Asp	Ser	Asp	Ala	Thr	Thr	Asp	Ala	His	Ile
				405					410					415	
Ile	Thr	Leu	Gly	Glu	Pro	Gly	Thr	Ser	Pro	Asn	Thr	Val	Phe	Ala	Ser
			420					425					430		
Asn	Gly	Leu	Tyr	Phe	Ala	Arg	Thr	Phe	His	Thr	Ser	Val	Val	Leu	Pro
		435					440					445			
Asp	Gly	Ser	Thr	Phe	Ile	Thr	Gly	Gly	Gln	Arg	Arg	Gly	Ile	Pro	Phe
	450					455					460				
Glu	Asp	Ser	Thr	Pro	Val	Phe	Thr	Pro	Glu	Ile	Tyr	Val	Pro	Glu	Gln
465					470					475					480
Asp	Thr	Phe	Tyr	Lys	Gln	Asn	Pro	Asn	Ser	Ile	Val	Arg	Ala	Tyr	His
				485					490					495	
Ser	Ile	Ser	Leu	Leu	Leu	Pro	Asp	Gly	Arg	Val	Phe	Asn	Gly	Gly	Gly
			500					505					510		
Gly	Leu	Cys	Gly	Asp	Cys	Thr	Thr	Asn	His	Phe	Asp	Ala	Gln	Ile	Phe
		515					520					525			
Thr	Pro	Asn	Tyr	Leu	Tyr	Asn	Ser	Asn	Gly	Asn	Leu	Ala	Thr	Arg	Pro
	530					535					540				
Lys	Ile	Thr	Arg	Thr	Ser	Thr	Gln	Ser	Val	Lys	Val	Gly	Gly	Arg	Ile
545					550					555					560
Thr	Ile	Ser	Thr	Asp	Ser	Ser	Ile	Ser	Lys	Ala	Ser	Leu	Ile	Arg	Tyr
				565					570					575	
Gly	Thr	Ala	Thr	His	Thr	Val	Asn	Thr	Asp	Gln	Arg	Arg	Ile	Pro	Leu
			580					585					590		
Thr	Leu	Thr	Asn	Asn	Gly	Gly	Asn	Ser	Tyr	Ser	Phe	Gln	Val	Pro	Ser

	595		600		605
Asp	Ser Gly Val Ala Leu Pro Gly Tyr Trp Met Leu Phe Val Met Asn				
610		615		620	
Ser	Ala Gly Val Pro Ser Val Ala Ser Thr Ile Arg Val Thr Gln				
625		630		635	

<210> 21
 <211> 639
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Mutant 4.F12 (N413D, S550, V494A, S610) from D.
 Dendroides GaO

<400> 21

Ala	Ser	Ala	Pro	Ile	Gly	Ser	Ala	Ile	Ser	Arg	Asn	Asn	Trp	Ala	Val
1				5					10					15	
Thr	Cys	Asp	Ser	Ala	Gln	Ser	Gly	Asn	Glu	Cys	Asn	Lys	Ala	Ile	Asp
			20					25					30		
Gly	Asn	Lys	Asp	Thr	Phe	Trp	His	Thr	Phe	Tyr	Gly	Ala	Asn	Gly	Asp
		35					40					45			
Pro	Lys	Pro	Pro	His	Thr	Tyr	Thr	Ile	Asp	Met	Lys	Thr	Thr	Gln	Asn
	50					55					60				
Val	Asn	Gly	Leu	Ser	Met	Leu	Pro	Arg	Gln	Asp	Gly	Asn	Gln	Asn	Gly
65					70					75					80
Trp	Ile	Gly	Arg	His	Glu	Val	Tyr	Leu	Ser	Ser	Asp	Gly	Thr	Asn	Trp
				85					90					95	
Gly	Ser	Pro	Val	Ala	Ser	Gly	Ser	Trp	Phe	Ala	Asp	Ser	Thr	Thr	Lys
			100					105					110		
Tyr	Ser	Asn	Phe	Glu	Thr	Arg	Pro	Ala	Arg	Tyr	Val	Arg	Leu	Val	Ala
		115					120					125			
Ile	Thr	Glu	Ala	Asn	Gly	Gln	Pro	Trp	Thr	Ser	Ile	Ala	Glu	Ile	Asn
	130					135					140				
Val	Phe	Gln	Ala	Ser	Ser	Tyr	Thr	Ala	Pro	Gln	Pro	Gly	Leu	Gly	Arg
145					150					155					160
Trp	Gly	Pro	Thr	Ile	Asp	Leu	Pro	Ile	Val	Pro	Ala	Ala	Ala	Ala	Ile
				165					170					175	
Glu	Pro	Thr	Ser	Gly	Arg	Val	Leu	Met	Trp	Ser	Ser	Tyr	Arg	Asn	Asp
			180					185					190		
Ala	Phe	Gly	Gly	Ser	Pro	Gly	Gly	Ile	Thr	Leu	Thr	Ser	Ser	Trp	Asp
		195					200					205			
Pro	Ser	Thr	Gly	Ile	Val	Ser	Asp	Arg	Thr	Val	Thr	Val	Thr	Lys	His
	210					215					220				
Asp	Met	Phe	Cys	Pro	Gly	Ile	Ser	Met	Asp	Gly	Asn	Gly	Gln	Ile	Val
225					230					235					240
Val	Thr	Gly	Gly	Asn	Asp	Ala	Lys	Lys	Thr	Ser	Leu	Tyr	Asp	Ser	Ser
				245					250					255	
Ser	Asp	Ser	Trp	Ile	Pro	Gly	Pro	Asp	Met	Gln	Val	Ala	Arg	Gly	Tyr
			260					265					270		
Gln	Ser	Ser	Ala	Thr	Met	Ser	Asp	Gly	Arg	Val	Phe	Thr	Ile	Gly	Gly
			275				280					285			
Ser	Trp	Ser	Gly	Gly	Val	Phe	Glu	Lys	Asn	Gly	Glu	Val	Tyr	Ser	Pro

290	Ser	Ser	Lys	Thr	Trp	Thr	295	Ser	Leu	Pro	Asn	Ala	300	Lys	Val	Asn	Pro	Met
305						310						315						320
	Leu	Thr	Ala	Asp	Lys	Gln	Gly	Leu	Tyr	Arg	Ser	330	Asp	Asn	His	Ala	Trp	
					325													335
	Leu	Phe	Gly	Trp	Lys	Lys	Gly	Ser	Val	Phe	Gln	Ala	Gly	Pro	Ser	Thr		
					340													350
	Ala	Met	Asn	Trp	Tyr	Tyr	Thr	Ser	Gly	Ser	Gly	Asp	Val	Lys	Ser	Ala		
					355													365
	Gly	Lys	Arg	Gln	Ser	Asn	Arg	Gly	Val	Ala	Pro	Asp	Ala	Met	Cys	Gly		
					370													380
	Asn	Ala	Val	Met	Tyr	Asp	Ala	Val	Lys	Gly	Lys	Ile	Leu	Thr	Phe	Gly		
	385					390												400
	Gly	Ser	Pro	Asp	Tyr	Gln	Asp	Ser	Asp	Ala	Thr	Thr	Asp	Ala	His	Ile		
					405													415
	Ile	Thr	Leu	Gly	Glu	Pro	Gly	Thr	Ser	Pro	Asn	Thr	Val	Phe	Ala	Ser		
					420													430
	Asn	Gly	Leu	Tyr	Phe	Ala	Arg	Thr	Phe	His	Thr	Ser	Val	Val	Leu	Pro		
					435													445
	Asp	Gly	Ser	Thr	Phe	Ile	Thr	Gly	Gly	Gln	Arg	Arg	Gly	Ile	Pro	Phe		
																		460
	Glu	Asp	Ser	Thr	Pro	Val	Phe	Thr	Pro	Glu	Ile	Tyr	Val	Pro	Glu	Gln		
	465					470												480
	Asp	Thr	Phe	Tyr	Lys	Gln	Asn	Pro	Asn	Ser	Ile	Val	Arg	Ala	Tyr	His		
					485													495
	Ser	Ile	Ser	Leu	Leu	Pro	Asp	Gly	Arg	Val	Phe	Asn	Gly	Gly	Gly			
					500													510
	Gly	Leu	Cys	Gly	Asp	Cys	Thr	Thr	Asn	His	Phe	Asp	Ala	Gln	Ile	Phe		
					515													525
	Thr	Pro	Asn	Tyr	Leu	Tyr	Asn	Ser	Asn	Gly	Asn	Leu	Ala	Thr	Arg	Pro		
																		540
	Lys	Ile	Thr	Arg	Thr	Ser	Thr	Gln	Ser	Val	Lys	Val	Gly	Gly	Arg	Ile		
	545					550												560
	Thr	Ile	Ser	Thr	Asp	Ser	Ser	Ile	Ser	Lys	Ala	Ser	Leu	Ile	Arg	Tyr		
					565													575
	Gly	Thr	Ala	Thr	His	Thr	Val	Asn	Thr	Asp	Gln	Arg	Arg	Ile	Pro	Leu		
					580													590
	Thr	Leu	Thr	Asn	Asn	Gly	Gly	Asn	Ser	Tyr	Ser	Phe	Gln	Val	Pro	Ser		
					595													605
	Asp	Ser	Gly	Val	Ala	Leu	Pro	Gly	Tyr	Trp	Met	Leu	Phe	Val	Met	Asn		
						615												620
	Ser	Ala	Gly	Val	Pro	Ser	Val	Ala	Ser	Thr	Ile	Arg	Val	Thr	Gln			
	625					630												635

<210> 22
 <211> 10
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Vector sequence

<400> 22

aagctagctt		10
<210> 23		
<211> 10		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Vector sequence		
<400> 23		
ttcgatcgaa		10
<210> 24		
<211> 10		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Vector sequence		
<400> 24		
gaattaattc		10
<210> 25		
<211> 10		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Vector sequence		
<400> 25		
cttaattaag		10
<210> 26		
<211> 9		
<212> PRT		
<213> Dactylium dendroides		
<400> 26		
Met Ala Ser Ala Pro Ile Gly Ser Ala		
1 5		
<210> 27		
<211> 27		
<212> DNA		
<213> Dactylium dendroides		
<400> 27		
atggcctcag cacctatcgg aagcgcc		27
<210> 28		

<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<221> unsure
<222> (1)...(27)
<223> "n" at positions 6, 9, 12, 15, and 21 is either a,
t, g, or c.
"n" at position 18 is either a, t, or c.

<223> Randomly altered D. Dendoides wild-type sequence

<400> 28
atggcntcng cncnatngg nagcgcc

27

<210> 29
<211> 14
<212> DNA
<213> Artificial Sequence

<220>
<223> Vector sequence

<400> 29
aggaaaagct tatg

14

<210> 30
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Vector sequence

<400> 30
aggaaaaagc ttatg

15

<210> 31
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Vector sequence

<400> 31
aggaaacaag cttatg

16

<210> 32
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
 <223> Vector sequence

<400> 32
 aggaacaaag cttatg 16

<210> 33
 <211> 14
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Vector sequence

<400> 33
 aggaaaagct tatg 14

<210> 34
 <211> 15
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Vector sequence

<400> 34
 aggaaaaagc ttatg 15

<210> 35
 <211> 16
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Vector sequence

<400> 35
 aggaacaag cttatg 16

<210> 36
 <211> 16
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Vector sequence

<400> 36
 aggaacaaag cttatg 16

<210> 37
 <211> 1917

<212> DNA

<213> Artificial Sequence

<220>

<223> Mutant 9.16.8D2 (A1609G) of D. Dendroides GaO

<400> 37

gcctcagcac	ctatcggaag	cgccatttct	cgcaacaact	gggccggtcac	ttgcgacagt	60
gcacagtcgg	gaaatgaatg	caacaaggcc	attgatggca	acaaggatac	cttttggcac	120
acattctatg	gcgccaacgg	ggatccaaag	ccccctcaca	catacacgat	tgacatgaag	180
acaactcaga	acgtcaacgg	cttgtctatg	ctgcctcgac	aggatggtaa	ccaaaacggc	240
tggatcggtc	gccatgaggt	ttatctaagc	tcagatggca	caaactgggg	cagccctggt	300
gcgtcaggta	gttggttcgc	cgactctact	acaaaatact	ccaactttga	aactcgccct	360
gctcgctatg	ttcgtcttgt	cgctatcact	gaagcgaatg	gccagccttg	gactagcatt	420
gcagagatca	acgtcttcca	agctagtctt	tacacagccc	cccagcctgg	tcttggacgc	480
tgggggtccga	ctattgactt	accgattggt	cctgcggctg	cagcaattga	accgacatcg	540
ggacgagtc	ttatgtggtc	ttcatatcgc	aatgatgcat	ttggaggatc	ccctgggtggt	600
atcactttga	cgtcttctg	ggatccatcc	actgggtattg	tttccgaccg	cactgtgaca	660
gtcaccaagc	atgatatggt	ctgccctggt	atctccatgg	atggtaacgg	tcagatcgta	720
gtcacagggtg	gcaacgatgc	caagaagacc	agtttgtatg	attcatctag	cgatagctgg	780
atcccgggac	ctgacatgca	agtggctcgt	gggtatcagt	catcagctac	catgtcagac	840
ggtcgtgttt	ttaccattgg	aggctcctgg	agcgggtggcg	tatttgagaa	gaatggcgaa	900
gtctatagcc	catcttcaaa	gacatggacg	tccctaccca	atgccaaagg	caacccaatg	960
ttgacggctg	acaagcaagg	attgtaccgt	tcagacaacc	acgcgtggct	ctttggatgg	1020
aagaagggtt	cggtgttcca	agcgggacct	agcacagcca	tgaactggta	ctataccagt	1080
ggaagtgggtg	atgtgaagtc	agccggaaaa	cgccagtcta	accgtgggtg	agccccctgat	1140
gccatgtgcg	gaaacgctgt	catgtacgac	gccgttaaag	gaaagatcct	gacctttggc	1200
ggctccccag	attatcaaga	ctctgacgcc	acaaccaacg	cccacatcat	caccctcggt	1260
gaacccggaa	catctcccaa	cactgtcttt	gctagcaatg	ggttgtactt	tgcccgaacg	1320
tttcacacct	ctgttggtct	tccagacgga	agcacgttta	ttacaggagg	ccaacgacgt	1380
ggaattccgt	tcgaggattc	aaccccggtg	tttacacctg	agatctacgt	ccctgaacaa	1440
gacactttct	acaagcagaa	ccccaaactcc	attgttcgcg	tctaccatag	catttccctt	1500
ttgttacctg	atggcaggggt	atttaacggt	gggtggtggc	tttgtggcga	ttgtaccacg	1560
aatcattttcg	acgcgcaaat	ctttacgcc	aactatcttt	acaatagcga	cggcaatctc	1620
gcgacacgtc	ccaagattac	cagaacctct	acacagagcg	tcaagggtcgg	tggcagaatt	1680
acaatctcga	cggattcttc	gattagcaag	gcgtcggttg	ttcgctatgg	tacagcgaca	1740
cacacgggta	atactgacca	gcgcgcgatt	cccctgactc	tgacaaacaa	tggaggaaat	1800
agctattctt	tccaagttcc	tagecactct	gggtgttgctt	tgcttggtta	ctggatgttg	1860
ttcgtgatga	actcggccgg	tgttcctagt	gtggcttcga	cgattcgcgt	tactcag	1917

<210> 38

<211> 1917

<212> DNA

<213> Artificial Sequence

<220>

<223> Mutant 9.16.6C11 (T1481C, T1543A) of D. Dendroides
GaO

<400> 38

gcctcagcac	ctatcggaag	cgccatttct	cgcaacaact	gggccggtcac	ttgcgacagt	60
gcacagtcgg	gaaatgaatg	caacaaggcc	attgatggca	acaaggatac	cttttggcac	120
acattctatg	gcgccaacgg	ggatccaaag	ccccctcaca	catacacgat	tgacatgaag	180

acaactcaga	acgtcaacgg	cttgtctatg	ctgcctcgac	aggatggtaa	ccaaaacggc	240
tggatcggtc	gccatgaggt	ttatctaagc	tcagatggca	caaactgggg	cagccctggt	300
gcgtcaggta	gttggttcgc	cgactctact	acaaaatact	ccaactttga	aactcgcctt	360
gctcgctatg	ttcgtcttgt	cgctatcact	gaagcgaatg	gccagccttg	gactagcatt	420
gcagagatca	acgtcttcca	agctagtctt	tacacagccc	cccagcctgg	tcttggacgc	480
tgggggtccga	ctattgactt	accgattggt	cctgcggctg	cagcaattga	accgacatcg	540
ggacgagtc	ttatgtgggc	ttcatatcgc	aatgatgcat	ttggaggatc	ccctgggtggt	600
atcactttga	cgtcttcctg	ggatccatcc	actggtattg	tttccgaccg	cactgtgaca	660
gtcaccaagc	atgatatggt	ctgccctggt	atctccatgg	atggtaacgg	tcagatcgta	720
gtcacagggtg	gcaacgatgc	caagaagacc	agtttgatg	attcatctag	cgatagctgg	780
atcccgggac	ctgacatgca	agtggctcgt	gggtatcagt	catcagctac	catgtcagac	840
ggtcgtgttt	ttaccattgg	aggctcctgg	agcgggtggc	tatttgagaa	gaatggcgaa	900
gtctatagcc	catcttcaaa	gacatggacg	tccctaccca	atgccaaagg	caaccctaag	960
ttgacggctg	acaagcaagg	attgtaccgt	tcagacaacc	acgcgtgggt	ctttggatgg	1020
aagaagggtt	cggtgttcca	agcgggacct	agcacagcca	tgaactggta	ctataccagt	1080
ggaagtgggtg	atgtgaagtc	agccggaaaa	cgccagtcta	accgtgggtg	agcccctgat	1140
gccatgtgcg	gaaacgctgt	catgtacgac	gccgttaaag	gaaagatcct	gacctttggc	1200
ggctccccag	attatcaaga	ctctgacgcc	acaaccaacg	cccacatcat	caccctcggt	1260
gaaccgggaa	catctcccaa	cactgtcttt	gctagcaatg	ggttgtactt	tgcccgaacg	1320
tttcacacct	ctggtgttct	tccagacgga	agcacgttta	ttacaggagg	ccaacgacgt	1380
ggaattccgt	tcgaggattc	aaccccggta	tttacacctg	agatctacgt	ccctgaacaa	1440
gacactttct	acaagcagaa	ccccaaactcc	attgttcgcg	cctaccatag	catttccctt	1500
ttgttacctg	atggcagggt	atttaacggt	ggtggtgggc	ttagtggcga	ttgtaccacg	1560
aatcatttcg	acgcgc aaat	ctttacgcc	aactatcttt	acaatagcaa	cggcaatctc	1620
gcgacacgtc	ccaagattac	cagaacctct	acacagagcg	tcaaggtcgg	tggcagaatt	1680
acaatctcga	cggattcttc	gattagcaag	gcgtcgttga	ttcgctatgg	tacagcgaca	1740
cacacgggta	atactgacca	gcgccgcatt	cccctgactc	tgacaaacaa	tggaggaaat	1800
agctattctt	tccaagttcc	tagcgactct	ggtgttgctt	tgcctggcta	ctggatgttg	1860
ttcgtgatga	actcggccgg	tgttcctagt	gtggcttcga	cgattcgcgt	tactcag	1917

<210> 39

<211> 1917

<212> DNA

<213> Artificial Sequence

<220>

<223> Mutant 9.16.16D12 (T408C, T1481C) of D. Dendroides
GaO

<400> 39

gcctcagcac	ctatcggaag	cgccattttct	cgcaacaact	gggccgtcac	ttgcgacagt	60
gcacagtcgg	gaaatgaatg	caacaaggcc	attgatggca	acaaggatac	cttttggcac	120
acattctatg	gcgccaacgg	ggatccaaag	ccccctcaca	catacacgat	tgacatgaag	180
acaactcaga	acgtcaacgg	cttgtctatg	ctgcctcgac	aggatggtaa	ccaaaacggc	240
tggatcggtc	gccatgaggt	ttatctaagc	tcagatggca	caaactgggg	cagccctggt	300
gcgtcaggta	gttggttcgc	cgactctact	acaaaatact	ccaactttga	aactcgcctt	360
gctcgctatg	ttcgtcttgt	cgctatcact	gaagcgaatg	gccagccctg	gactagcatt	420
gcagagatca	acgtcttcca	agctagtctt	tacacagccc	cccagcctgg	tcttggacgc	480
tgggggtccga	ctattgactt	accgattggt	cctgcggctg	cagcaattga	accgacatcg	540
ggacgagtc	ttatgtgggc	ttcatatcgc	aatgatgcat	ttggaggatc	ccctgggtggt	600
atcactttga	cgtcttcctg	ggatccatcc	actggtattg	tttccgaccg	cactgtgaca	660
gtcaccaagc	atgatatggt	ctgccctggt	atctccatgg	atggtaacgg	tcagatcgta	720
gtcacagggtg	gcaacgatgc	caagaagacc	agtttgatg	attcatctag	cgatagctgg	780

atccccgggac	ctgacatgca	agtggctcgt	gggtatcagt	catcagctac	catgtcagac	840
ggtcgtgttt	ttaccattgg	aggctcctgg	agcgggtggcg	tatttgagaa	gaatggcgaa	900
gtctatagcc	catcttcaaa	gacatggacg	tccctaccca	atgccaaagg	caacccaatg	960
ttgacggctg	acaagcaagg	attgtaccgt	tcagacaacc	acgcgtggct	ctttggatgg	1020
aagaagggtt	cggtgttcca	agcgggacct	agcacagcca	tgaactggta	ctataccagt	1080
ggaagtgggtg	atgtgaagtc	agccggaaaa	cgccagtcta	accgtgggtg	agccccctgat	1140
gccatgtgcg	gaaacgctgt	catgtacgac	gccgttaaag	gaaagatcct	gacctttggc	1200
ggctccccag	attatcaaga	ctctgacgcc	acaaccaacg	cccacatcat	caccctcggt	1260
gaacccggaa	catctcccaa	cactgtcttt	gctagcaatg	ggttgtactt	tgcccgaacg	1320
tttcacacct	ctgttggttct	tccagacgga	agcacgttta	ttacaggagg	ccaacgacgt	1380
ggaattccgt	tcgaggattc	aaccccggtg	tttacacctg	agatctacgt	ccctgaacaa	1440
gacactttct	acaagcagaa	ccccaaactcc	attgttcgcg	cctaccatag	catttccctt	1500
ttgttacctg	atggcagggt	atttaacggg	gggtgggtggtc	tttgtggcga	ttgtaccacg	1560
aatcattttcg	acgcgcgaaat	ctttacgcca	aactatcttt	acaatagcaa	cggcaatctc	1620
gcgacacgtc	ccaagattac	cagaacctct	acacagagcg	tcaagggtcg	tggcagaatt	1680
acaatctcga	cggattcttc	gattagcaag	gcgtcggttg	ttcgctatgg	tacagcgaca	1740
cacacgggta	atactgacca	gcgcgcgatt	cccctgactc	tgacaaacaa	tggagggaat	1800
agctattctt	tccaagttcc	tagcgactct	gggtgttgctt	tgcttggtta	ctggatgttg	1860
ttcgtgatga	actcggccgg	tgttcctagt	gtggcttcga	cgattcgcgt	tactcag	1917

<210> 40

<211> 1917

<212> DNA

<213> Artificial Sequence

<220>

<223> Mutant 11.03.6D3 (T28C, T408C, T1481C) of D.
Dendroides GaO

<400> 40

gcctcagcac	ctatcggaag	cgccattcct	cgcaacaact	gggccgtcac	ttgcgacagt	60
gcacagtcgg	gaaatgaatg	caacaaggcc	attgatggca	acaaggatac	cttttggcac	120
acattctatg	gcgccaacgg	ggatccaaag	ccccctcaca	catacacgat	tgacatgaag	180
acaactcaga	acgtcaacgg	cttgtctatg	ctgcctcgac	aggatggtaa	ccaaaacggc	240
tggatcgggtc	gccatgaggt	ttatctaagc	tcagatggca	caaactgggg	cagccctggt	300
gcgtcaggta	gttgggttcgc	cgactctact	acaaaatact	ccaactttga	aactcgcctt	360
gctcgctatg	ttcgtcttgt	cgctatcact	gaagcgaatg	gccagccctg	gactagcatt	420
gcagagatca	acgtcttcca	agctagttct	tacacagccc	cccagcctgg	tcttggacgc	480
tgggggtccga	ctattgactt	accgattggt	cctgcggctg	cagcaattga	accgacatcg	540
ggacgagtc	ttatgtgggtc	ttcatatcgc	aatgatgcat	ttggaggatc	ccctgggtggt	600
atcactttga	cgtcttctctg	ggatccatcc	actggtattg	tttccgaccg	cactgtgaca	660
gtcaccaagc	atgatatggt	ctgccctggt	atctccatgg	atggtaacgg	tcagatcgta	720
gtcacagggtg	gcaacgatgc	caagaagacc	agtttgatg	attcatctag	cgatagctgg	780
atccccgggac	ctgacatgca	agtggctcgt	gggtatcagt	catcagctac	catgtcagac	840
ggtcgtgttt	ttaccattgg	aggctcctgg	agcgggtggcg	tatttgagaa	gaatggcgaa	900
gtctatagcc	catcttcaaa	gacatggacg	tccctaccca	atgccaaagg	caacccaatg	960
ttgacggctg	acaagcaagg	attgtaccgt	tcagacaacc	acgcgtggct	ctttggatgg	1020
aagaagggtt	cggtgttcca	agcgggacct	agcacagcca	tgaactggta	ctataccagt	1080
ggaagtgggtg	atgtgaagtc	agccggaaaa	cgccagtcta	accgtgggtg	agccccctgat	1140
gccatgtgcg	gaaacgctgt	catgtacgac	gccgttaaag	gaaagatcct	gacctttggc	1200
ggctccccag	attatcaaga	ctctgacgcc	acaaccaacg	cccacatcat	caccctcggt	1260
gaacccggaa	catctcccaa	cactgtcttt	gctagcaatg	ggttgtactt	tgcccgaacg	1320
tttcacacct	ctgttggttct	tccagacgga	agcacgttta	ttacaggagg	ccaacgacgt	1380

ggaattccgt	tcgaggattc	aacccccggt	tttacacctg	agatctacgt	ccctgaacaa	1440
gacactttct	acaagcagaa	cccccaactcc	attgttcgcg	cctaccatag	catttccctt	1500
ttgttacctg	atggcagggg	atttaacggg	ggtggtgggc	tttgtggcga	ttgtaccacg	1560
aatcatttct	acgcgcaa	ctttacgcca	aactatcttt	acaatagcaa	cggcaatctc	1620
gcgacacgtc	ccaagattac	cagaacctct	acacagagcg	tcaagggtcgg	tggcagaatt	1680
acaatctcga	cggattcttc	gattagcaag	gcgtcgttga	ttcgctatgg	tacagcgaca	1740
cacacgggta	atactgacca	gcgcgcgatt	cccctgactc	tgacaaacaa	tggaggaaat	1800
agctattctt	tccaagttcc	tagcgactct	ggtgttgctt	tgccctggcta	ctggatgttg	1860
ttcgtgatga	actcggccgg	tggttcctagt	gtggcttcga	cgattcgcgt	tactcag	1917

<210> 41

<211> 1917

<212> DNA

<213> Artificial Sequence

<220>

<223> Mutant 11.03.10C3 (A9C, T408C, G584A, T1481C) of
D. Dendroides GaO

<400> 41

gcctcagccc	ctatcggaag	cgccatttct	cgcaacaact	gggccgctcac	ttgcgacagt	60
gcacagtcgg	gaaatgaatg	caacaaggcc	attgatggca	acaaggatac	cttttggcac	120
acatttctatg	gcgccaacgg	ggatccaaag	ccccctcaca	catacacgat	tgacatgaag	180
acaactcaga	acgtcaacgg	cttgtctatg	ctgcctcgac	aggatggtaa	ccaaaacggc	240
tggatcggtc	gccatgaggt	ttatctaagc	tcagatggca	caaactgggg	cagccctggt	300
gcgtcaggta	gttggttcgc	cgactctact	acaaaatact	ccaactttga	aactcgcctt	360
gctcgtctatg	ttcgtcttgt	cgctatcact	gaagcgaatg	gccagccctg	gactagcatt	420
gcagagatca	acgtcttcca	agctagtctt	tacacagccc	cccagcctgg	tcttggacgc	480
tggggtcgga	ctattgactt	accgattggt	cctgcggctg	cagcaattga	accgacatcg	540
ggacgagtc	ttatgtgggc	ttcatatcgc	aatgatgc	ttgaaggatc	ccctgggtggt	600
atcactttga	cgtcttcctg	ggatccatcc	actggtattg	tttccgaccg	cactgtgaca	660
gtcaccaagc	atgatatggt	ctgccttggt	atctccatgg	atggtaacgg	tcagatcgta	720
gtcacagggtg	gcaacgatgc	caagaagacc	agtttgtatg	attcatctag	cgatagctgg	780
atcccggggac	ctgacatgca	agtggctcgt	gggtatcagt	catcagctac	catgtcagac	840
ggctcgtgttt	ttaccattgg	aggctcctgg	agcgggtggc	tatttgagaa	gaatggcgaa	900
gtctatagcc	catcttcaaa	gacatggacg	tccctacceca	atgccaaagg	caacccaatg	960
ttgacgggctg	acaagcaagg	attgtaccgt	tcagacaacc	acgcgtgggt	ctttggatgg	1020
aagaaggggtt	cgggtgttcca	agcggggacct	agcacagcca	tgaactggta	ctataccagt	1080
ggaagtgggtg	atgtgaagtc	agccggaaaa	cgccagtc	accgtgggtg	agccccctgat	1140
gccatgtgcg	gaaacgctgt	catgtacgac	gccgttaaag	gaaagatcct	gacctttggc	1200
ggctccccag	attatcaaga	ctctgacgcc	acaaccaacg	cccacatcat	caccctcggt	1260
gaacccggaa	catctcccaa	cactgtcttt	gctagcaatg	ggttgtactt	tgcccgaacg	1320
tttcacacct	ctgttggtct	tccagacgga	agcacgttta	ttacaggagg	ccaacgacgt	1380
ggaattccgt	tcgaggattc	aacccccggt	tttacacctg	agatctacgt	ccctgaacaa	1440
gacactttct	acaagcagaa	cccccaactcc	attgttcgcg	cctaccatag	catttccctt	1500
ttgttacctg	atggcagggg	atttaacggg	ggtggtgggc	tttgtggcga	ttgtaccacg	1560
aatcatttct	acgcgcaa	ctttacgcca	aactatcttt	acaatagcaa	cggcaatctc	1620
gcgacacgtc	ccaagattac	cagaacctct	acacagagcg	tcaagggtcgg	tggcagaatt	1680
acaatctcga	cggattcttc	gattagcaag	gcgtcgttga	ttcgctatgg	tacagcgaca	1740
cacacgggta	atactgacca	gcgcgcgatt	cccctgactc	tgacaaacaa	tggaggaaat	1800
agctattctt	tccaagttcc	tagcgactct	ggtgttgctt	tgccctggcta	ctggatgttg	1860
ttcgtgatga	actcggccgg	tggttcctagt	gtggcttcga	cgattcgcgt	tactcag	1917

<210> 42
 <211> 1917
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Mutant 11.03.10D6 (T408C, T654C, A936G, T1481C, A1603G) of D. Dendroides GaO

<400> 42

gcctcagcac	ctatcggaag	cgccatttct	cgcaacaact	gggccggtcac	ttgcgacagt	60
gcacagtcgg	gaaatgaatg	caacaaggcc	attgatggca	acaaggatac	cttttggcac	120
acattctatg	gcgccaacgg	ggatccaaag	ccccctcaca	catacacgat	tgacatgaag	180
acaactcaga	acgtcaacgg	cttgtctatg	ctgcctcgac	aggatggtaa	ccaaaacggc	240
tggatcgggc	gccatgaggt	ttatctaagc	tcagatggca	caaactgggg	cagccctggt	300
gcgtcaggta	gttgggttcgc	cgactctact	acaaaatact	ccaactttga	aactcgccct	360
gctcgctatg	ttcgtcttgt	cgctatcact	gaagcgaatg	gccagccctg	gactagcatt	420
gcagagatca	acgtcttcca	agctagttct	tacacagccc	cccagccctg	tcttggacgc	480
tgggggtccga	ctattgactt	accgattggt	cctgcggctg	cagcaattga	accgacatcg	540
ggacgagtc	ttatgtgggc	ttcatatcgc	aatgatgcat	ttggaggatc	ccctgggtggt	600
atcactttga	cgtcttccctg	ggatccatcc	actggtattg	tttccgaccg	caccgtgaca	660
gtcaccaagc	atgatatggt	ctgccttggt	atctccatgg	atggtaacgg	tcagatcgta	720
gtcacagggtg	gcaacgatgc	caagaagacc	agtttgtatg	attcatctag	cgatagctgg	780
atcccggggac	ctgacatgca	agtggctcgt	gggtatcagt	catcagctac	catgtcagac	840
ggtcgtgttt	ttaccattgg	aggctcctgg	agcgggtggcg	tatttgagaa	gaatggcgaa	900
gtctatagcc	catcttcaaa	gacatggacg	tccctgccca	atgccaaagg	caacccaatg	960
ttgacggctg	acaagcaagg	attgtaccgt	tcagacaacc	acgcgtggct	ctttggatgg	1020
aagaagggtt	cgggtgttcca	agcgggacct	agcacagcca	tgaactggta	ctataccagt	1080
ggaagtgggtg	atgtgaagtc	agccggaaaa	cgccagtcta	accgtgggtg	agccctgat	1140
gccatgtgcg	gaaacgctgt	catgtacgac	gccgttaaag	gaaagatcct	gacctttggc	1200
ggctccccag	attatcaaga	ctctgacgcc	acaaccaacg	cccacatcat	caccctcggt	1260
gaacccggaa	catctcccaa	cactgtcttt	gctagcaatg	ggttgtactt	tgcccgaacg	1320
tttcacacct	ctgttggttct	tccagacgga	agcacgttta	ttacaggagg	ccaacgacgt	1380
ggaattccgt	tcgaggattc	aaccccggta	tttacacctg	agatctacgt	ccctgaacaa	1440
gacactttct	acaagcagaa	ccccaaactcc	attgttcgcg	cctaccatag	catttccctt	1500
ttgttacctg	atggcaggggt	atttaacgggt	gggtgggtggtc	tttgtggcga	ttgtaccacg	1560
aatcattttcg	acgcgcaa	ctttacgcca	aactatcttt	acgatagcaa	cggcaatctc	1620
gcgacacgtc	ccaagattac	cagaacctct	acacagagcg	tcaagggtcgg	tggcagaatt	1680
acaatctcga	cggattcttc	gattagcaag	gcgtcggttg	ttcgctatgg	tacagcgaca	1740
cacacgggtta	atactgacca	gcgcgcgatt	cccctgactc	tgacaaacaa	tggaggaaat	1800
agctatttctt	tccaagttcc	tagcgactct	gggtgttgctt	tgcttggtcta	ctggatgttg	1860
ttcgtgatga	actcggccgg	tgttcctagt	gtggcttcga	cgattcgcgt	tactcag	1917

<210> 43
 <211> 1917
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Mutant 11.03.13E12 (A208G, T408C, T1481C) of D. Dendroides GaO

<400> 43

gcctcagcac	ctatcggaag	cgccatttct	cgcaacaact	gggccggtcac	ttgcgacagt	60
gcacagtcgg	gaaatgaatg	caacaaggcc	attgatggca	acaaggatac	cttttggcac	120
acattctatg	gcgccaacgg	ggatccaaag	ccccctcaca	catacacgat	tgacatgaag	180
acaactcaga	acgtcaacgg	cttgtctgtg	ctgcctcgac	aggatggtaa	ccaaaacggc	240
tggatcggtc	gccatgaggt	ttatctaagc	tcagatggca	caaactgggg	cagccctggt	300
gcgtcaggta	gttggttcgc	cgactctact	acaaaatact	ccaactttga	aactcgccct	360
gctcgctatg	ttcgtcttgt	cgctatcact	gaagcgaatg	gccagccctg	gactagcatt	420
gcagagatca	acgtcttcca	agctagtctt	tacacagccc	cccagcctgg	tcttggacgc	480
tgggggtccga	ctattgactt	accgattggt	cctgcggctg	cagcaattga	accgacatcg	540
ggacgagtc	ttatgtggtc	ttcatatcgc	aatgatgcat	ttggaggatc	ccctgggtggt	600
atcactttga	cgtcttctg	ggatccatcc	actggtattg	tttccgaccg	cactgtgaca	660
gtcaccaagc	atgatatggt	ctgccctggg	atctccatgg	atggtaacgg	tcagatcgta	720
gtcacaggtg	gcaacgatgc	caagaagacc	agtttgtatg	attcatctag	cgatagctgg	780
atcccgggac	ctgacatgca	agtggctcgt	gggtatcagt	catcagctac	catgtcagac	840
ggtcgtgttt	ttaccattgg	aggctcctgg	agcgggtggcg	tatttgagaa	gaatggcgaa	900
gtctatagcc	catcttcaaa	gacatggacg	tccctaccca	atgccaaagt	caacccaatg	960
ttgacggctg	acaagcaagg	attgtaccgt	tcagacaacc	acgcgtggct	ctttggatgg	1020
aagaagggtt	cggtgttcca	agcgggacct	agcacagcca	tgaactggta	ctataccagt	1080
ggaagtgggtg	atgtgaagtc	agccggaaaa	cgccagtcta	accgtgggtg	agccctgat	1140
gccatgtgcg	gaaacgctgt	catgtacgac	gccgttaaag	gaaagatcct	gacctttggc	1200
ggctccccag	attatcaaga	ctctgacgcc	acaaccaacg	cccacatcat	cacctcggt	1260
gaacccggaa	catctcccaa	cactgtcttt	gctagcaatg	ggttgtactt	tgcccgaacg	1320
tttcacacct	ctgttgttct	tccagacgga	agcacgttta	ttacaggagg	ccaacgacgt	1380
ggaattccgt	togaggattc	aaccccggta	tttacacctg	agatctacgt	ccctgaacaa	1440
gacactttct	acaagcagaa	ccccaaactcc	attgttcgcg	cctaccatag	catttccctt	1500
ttgttacctg	atggcagggg	atttaacggg	gggtgggtggtc	tttgtggcga	ttgtaccacg	1560
aatcattttcg	acgcgcaaat	ctttacgcc	aactatcttt	acaatagcaa	cggcaatctc	1620
gcgacacgtc	ccaagattac	cagaacctct	acacagagcg	tcaaggtcgg	tggcagaatt	1680
acaatctcga	cggattcttc	gattagcaag	gcgtcgttga	ttcgctatgg	tacagcgaca	1740
cacacgggta	atactgacca	gcgccgcatt	cccctgactc	tgacaaacaa	tggaggaaat	1800
agctattctt	tccaagttcc	tagcgactct	gggtgttgctt	tgcttggtta	ctggatgttg	1860
ttcgtgatga	actcggccgg	tgttcctagt	gtggcttcga	cgattcgcgt	tactcag	1917

<210> 44

<211> 1917

<212> DNA

<213> Artificial Sequence

<220>

<223> Mutant 1.06.20E7 (T28C, A208G, T408C, G584A,
T1481C, A1603G) of D. Dendroides GaO

<400> 44

gcctcagcac	ctatcggaag	cgccattcct	cgcaacaact	gggccggtcac	ttgcgacagt	60
gcacagtcgg	gaaatgaatg	caacaaggcc	attgatggca	acaaggatac	cttttggcac	120
acattctatg	gcgccaacgg	ggatccaaag	ccccctcaca	catacacgat	tgacatgaag	180
acaactcaga	acgtcaacgg	cttgtctgtg	ctgcctcgac	aggatggtaa	ccaaaacggc	240
tggatcggtc	gccatgaggt	ttatctaagc	tcagatggca	caaactgggg	cagccctggt	300
gcgtcaggta	gttggttcgc	cgactctact	acaaaatact	ccaactttga	aactcgccct	360
gctcgctatg	ttcgtcttgt	cgctatcact	gaagcgaatg	gccagccctg	gactagcatt	420
gcagagatca	acgtcttcca	agctagtctt	tacacagccc	cccagcctgg	tcttggacgc	480
tgggggtccga	ctattgactt	accgattggt	cctgcggctg	cagcaattga	accgacatcg	540
ggacgagtc	ttatgtggtc	ttcatatcgc	aatgatgcat	ttgaaggatc	ccctgggtggt	600

atcactttga	cgtcttctctg	ggatccatcc	actggtattg	tttccgaccg	cactgtgaca	660
gtcaccaagc	atgatatgtt	ctgccctggt	atctccatgg	atggtaacgg	tcagatcgta	720
gtcacagggtg	gcaacgatgc	caagaagacc	agtttgtatg	attcatctag	cgatagctgg	780
atcccggggac	ctgacatgca	agtggctcgt	gggtatcagt	catcagctac	catgtcagac	840
ggtcgtgttt	ttaccattgg	aggctcctgg	agcgggtggcg	tatttgagaa	gaatggcgaa	900
gtctatagcc	catcttcaaa	gacatggacg	tccctaccca	atgccaaagg	caacccaatg	960
ttgacggctg	acaagcaagg	attgtaccgt	tcagacaacc	acgcgtgggt	ctttggatgg	1020
aagaaggggtt	cgggtgttcca	agcggggacct	agcacagcca	tgaactggta	ctataccagt	1080
ggaagtgggtg	atgtgaagtc	agccggaaaa	cgccagtcta	accgtgggtg	agccccctgat	1140
gccatgtgcg	gaaacgctgt	catgtacgac	gccgttaaag	gaaagatcct	gacctttggc	1200
ggctccccag	attatcaaga	ctctgacgcc	acaaccaacg	cccacatcat	caccctcggt	1260
gaacccggaa	catctcccaa	cactgtcttt	gctagcaatg	ggttgtactt	tgcccgaaacg	1320
tttcacacct	ctgttggtct	tccagacgga	agcacgttta	ttacaggagg	ccaacgacgt	1380
ggaattccgt	tcgaggattc	aaccccggtg	tttacacctg	agatctacgt	ccctgaacaa	1440
gacactttct	acaagcagaa	ccccaaactcc	attgttcgcg	cctaccatag	catttccctt	1500
ttgttacctg	atggcagggt	atttaacggt	gggtggtggtc	tttgtggcga	ttgtaccacg	1560
aatcatttcg	acgcgcgaat	ctttacgcga	aactatcttt	acgatagcaa	cggcaatctc	1620
gcgacacgtc	ccaagattac	cagaacctct	acacagagcg	tcaaggtcgg	tggcagaatt	1680
acaatctcga	cggattcttc	gattagcaag	gcgtcgttga	ttcgctatgg	tacagcgaca	1740
cacacgggtta	atactgacca	gcgcgcgatt	cccttgactc	tgacaaacaa	tggaggaaat	1800
agctattctt	tccaagttcc	tagcgactct	ggtgttgctt	tgcttggtta	ctggatggtg	1860
ttcgtgatga	actcggcggg	tgttcctagt	gtggcttcga	cgattcgcgt	tactcag	1917

<210> 45

<211> 1917

<212> DNA

<213> Artificial Sequence

<220>

<223> Mutant 1.D4 (A1237G) of D. Dendroides GaO

<400> 45

gcctcagcac	ctatcggaag	cgccatttct	cgcaacaact	gggccgtcac	ttgcgacagt	60
gcacagtcgg	gaaatgaatg	caacaaggcc	attgatggca	acaaggatac	cttttggcac	120
acattctatg	gcgcacaacg	ggatccaaag	ccccctcaca	catacacgat	tgacatgaag	180
acaactcaga	acgtcaacgg	cttgtctatg	ctgcctcgac	aggatggtaa	ccaaaacggc	240
tggatcggtc	gccatgaggt	ttatctaagc	tcagatggca	caaactgggg	cagccctgtt	300
gcgtcaggta	gttggttcgc	cgactctact	acaaaatact	ccaactttga	aactcgcctt	360
gctcgctatg	ttcgtcttgt	cgctatcact	gaagcgaatg	gccagccttg	gactagcatt	420
gcagagatca	acgtcttcca	agctagtctt	tacacagccc	cccagcctgg	tcttggacgc	480
tgggggtccga	ctattgactt	accgattggt	cctgcggctg	cagcaattga	accgacatcg	540
ggacgagtc	ttatgtgggt	ttcatatcgc	aatgatgcat	ttggaggatc	ccctgggtggt	600
atcactttga	cgtcttctctg	ggatccatcc	actggtattg	tttccgaccg	cactgtgaca	660
gtcaccaagc	atgatatgtt	ctgccctggt	atctccatgg	atggtaacgg	tcagatcgta	720
gtcacagggtg	gcaacgatgc	caagaagacc	agtttgtatg	attcatctag	cgatagctgg	780
atcccggggac	ctgacatgca	agtggctcgt	gggtatcagt	catcagctac	catgtcagac	840
ggtcgtgttt	ttaccattgg	aggctcctgg	agcgggtggcg	tatttgagaa	gaatggcgaa	900
gtctatagcc	catcttcaaa	gacatggacg	tccctaccca	atgccaaagg	caacccaatg	960
ttgacggctg	acaagcaagg	attgtaccgt	tcagacaacc	acgcgtgggt	ctttggatgg	1020
aagaaggggtt	cgggtgttcca	agcggggacct	agcacagcca	tgaactggta	ctataccagt	1080
ggaagtgggtg	atgtgaagtc	agccggaaaa	cgccagtcta	accgtgggtg	agccccctgat	1140
gccatgtgcg	gaaacgctgt	catgtacgac	gccgttaaag	gaaagatcct	gacctttggc	1200
ggctccccag	attatcaaga	ctctgacgcc	acaaccgacg	cccacatcat	caccctcggt	1260

gaacccggaa	catctcccaa	cactgtcttt	gctagcaatg	ggttgtaact	tgcccgaacg	1320
tttcacacct	ctgttggttct	tccagacgga	agcacgttta	ttacaggagg	ccaacgacgt	1380
ggaattccgt	tcgaggattc	aaccccggtg	tttacacctg	agatctacgt	ccctgaacaa	1440
gacactttct	acaagcagaa	ccccaaactcc	attgttcgcg	tctaccatag	catttccctt	1500
ttgttacctg	atggcagggt	atttaacggt	ggtggtggtc	tttgtggcga	ttgtaccacg	1560
aatcattttcg	acgcgcgaaat	ctttacgcca	aactatcttt	acaatagcaa	cggcaatctc	1620
gcgacacgtc	ccaagattac	cagaacctct	acacagagcg	tcaagggtcg	tggcagaatt	1680
acaatctcga	cggattcttc	gattagcaag	gcgtcggtga	ttcgctatgg	tacagcgaca	1740
cacacgggta	atactgacca	gcgcgcgatt	cccctgactc	tgacaaacaa	tggaggaaat	1800
agctattctt	tccaagttcc	tagcgactct	ggtgttgctt	tgcttggtta	ctggatgttg	1860
ttcgtgatga	actcggccgg	tgttcctagt	gtggcttcga	cgattcgcgt	tactcag	1917

<210> 46

<211> 1917

<212> DNA

<213> Artificial Sequence

<220>

<223> Mutant 2.G4 (A1237G, T1650A) of D. Dendroides GaO

<400> 46

gcctcagcac	ctatcggaag	cgccattttct	cgcaacaact	gggccggtcac	ttgcgacagt	60
gcacagtcgg	gaaatgaatg	caacaaggcc	attgatggca	acaaggatac	cttttggcac	120
acattctatg	gcgccaacgg	ggatccaaag	ccccctcaca	catacacgat	tgacatgaag	180
acaactcaga	acgtcaacgg	cttgtctatg	ctgcctcgac	aggatggtaa	ccaaaacggc	240
tggatcggtc	gccatgaggt	ttatctaagc	tcagatggca	caaactgggg	cagccctggt	300
gcgtcaggta	gttggttcgc	cgactctact	acaaaatact	ccaactttga	aactcgcctt	360
gctcgctatg	ttcgtcttgg	cgctatcact	gaagcgaatg	gccagccttg	gactagcatt	420
gcagagatca	acgtcttcca	agctagtctt	tacacagccc	cccagcctgg	tcttggacgc	480
tgggggtccga	ctattgactt	accgattggt	cctgcggctg	cagcaattga	accgacatcg	540
ggacgagttc	ttatgtggtc	ttcatatcgc	aatgatgcat	ttggaggatc	ccctgggtggt	600
atcactttga	cgtcttccctg	ggatccatcc	actgggtattg	tttccgaccg	cactgtgaca	660
gtcaccaagc	atgatatggt	ctgccctggt	atctccatgg	atggtaacgg	tcagatcgta	720
gtcacagggtg	gcaacgatgc	caagaagacc	agtttgtatg	attcatctag	cgatagctgg	780
atcccggggac	ctgacatgca	agtggctcgt	gggtatcagt	catcagctac	catgtcagac	840
ggtcgtgttt	ttaccattgg	aggctcctgg	agcgggtggcg	tatttgagaa	gaatggcgaa	900
gtctatagcc	catcttcaaa	gacatggacg	tccttaccca	atgccaaagg	caacccaatg	960
ttgacgggctg	acaagcaagg	attgtaccgt	tcagacaacc	acgcgtggct	ctttggatgg	1020
aagaagggtt	cgggtgtcca	agcgggacct	agcacagcca	tgaactggta	ctataccagt	1080
ggaagtgggtg	atgtgaagtc	agccggaaaa	cgccagtcta	accgtgggtg	agcccctgat	1140
gccatgtgcg	gaaacgctgt	catgtacgac	gccgttaaag	gaaagatcct	gacctttggc	1200
ggctccccag	attatcaaga	ctctgacgcc	acaaccgacg	cccacatcat	caccctcggt	1260
gaacccggaa	catctcccaa	cactgtcttt	gctagcaatg	ggttgtaact	tgcccgaacg	1320
tttcacacct	ctgttggttct	tccagacgga	agcacgttta	ttacaggagg	ccaacgacgt	1380
ggaattccgt	tcgaggattc	aaccccggtg	tttacacctg	agatctacgt	ccctgaacaa	1440
gacactttct	acaagcagaa	ccccaaactcc	attgttcgcg	tctaccatag	catttccctt	1500
ttgttacctg	atggcagggt	atttaacggt	ggtggtggtc	tttgtggcga	ttgtaccacg	1560
aatcattttcg	acgcgcgaaat	ctttacgcca	aactatcttt	acaatagcaa	cggcaatctc	1620
gcgacacgtc	ccaagattac	cagaacctca	acacagagcg	tcaagggtcg	tggcagaatt	1680
acaatctcga	cggattcttc	gattagcaag	gcgtcggtga	ttcgctatgg	tacagcgaca	1740
cacacgggta	atactgacca	gcgcgcgatt	cccctgactc	tgacaaacaa	tggaggaaat	1800
agctattctt	tccaagttcc	tagcgactct	ggtgttgctt	tgcttggtta	ctggatgttg	1860
ttcgtgatga	actcggccgg	tgttcctagt	gtggcttcga	cgattcgcgt	tactcag	1917

<210> 47
 <211> 1917
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Mutant 3.H7 (A1237G, T1650A, T1481C) of D.
 Dendroides GaO

<400> 47

gcctcagcac	ctatcggaag	cgccatttct	cgcaacaact	gggccgtcac	ttgcgacagt	60
gcacagtcgg	gaaatgaatg	caacaaggcc	attgatggca	acaaggatac	cttttggcac	120
acattctatg	gcgccaacgg	ggatccaaag	ccccctcaca	catacacgat	tgacatgaag	180
acaactcaga	acgtcaacgg	cttgtctatg	ctgcctcgac	aggatggtaa	ccaaaacggc	240
tggatcgggtc	gccatgaggt	ttatctaagc	tcagatggca	caaactgggg	cagccctgtt	300
gcgtcaggta	gltggttcgc	cgactctact	acaaaataact	ccaactttga	aactcgcctt	360
gctcgctatg	ttcgtcttgt	cgctatcact	gaagcgaatg	gccagccttg	gactagcatt	420
gcagagatca	acgtcttcca	agctagtctt	tacacagccc	cccagcctgg	tcttggacgc	480
tggggtccga	ctattgactt	accgattgtt	cctgcggctg	cagcaattga	accgacatcg	540
ggacgagtc	ttatgtgggtc	ttcatatcgc	aatgatgcat	ttggaggatc	ccctgggtgt	600
atcactttga	cgtcttctctg	ggatccatcc	actgggtattg	tttccgaccg	cactgtgaca	660
gtcaccaagc	atgatatgtt	ctgccctggg	atctccatgg	atggtaacgg	tcagatcgta	720
gtcacagggtg	gcaacgatgc	caagaagacc	agtttgtatg	attcatctag	cgatagctgg	780
atcccgggac	ctgacatgca	agtggctcgt	gggtatcagt	catcagctac	catgtcagac	840
ggtcgtgttt	ttaccattgg	aggctcctgg	agcgggtggcg	tatttgagaa	gaatggcgaa	900
gtctatagcc	catcttcaaa	gacatggacg	tccctaccca	atgccaaagt	caacccaatg	960
ttgacggctg	acaagcaagg	attgtaccgt	tcagacaacc	acgcgtgggt	ctttggatgg	1020
aagaagggtt	cggtgttcca	agcgggacct	agcacagcca	tgaactggta	ctataccagt	1080
ggaagtgggtg	atgtgaagtc	agccggaaaa	cgccagtcct	accgtgggtg	agccccgat	1140
gccatgtgcg	gaaacgctgt	catgtacgac	gccgttaaag	gaaagatcct	gacctttggc	1200
ggctccccag	attatcaaga	ctctgacgcc	acaaccgacg	cccacatcat	caccctcggt	1260
gaacccggaa	catctcccaa	cactgtcttt	gctagcaatg	ggttgtactt	tgcccgaacg	1320
tttcacacct	ctgttggtct	tccagacgga	agcacgttta	ttacaggagg	ccaacgacgt	1380
ggaattccgt	tcgaggattc	aaccccggtg	tttacacctg	agatctacgt	ccctgaacaa	1440
gacactttct	acaagcagaa	ccccaaactcc	attgttcgcg	cctaccatag	catttccctt	1500
ttgttacctg	atggcagggt	atttaacggt	gggtgggtggtc	tttgtggcga	ttgtaccacg	1560
aatcatttcg	acgcgcaa	ctttacgcca	aactatcttt	acaatagcaa	cggcaatctc	1620
gcgacacgtc	ccaagattac	cagaacctca	acacagagcg	tcaaggctcg	tggcagaatt	1680
acaatctcga	cggattcttc	gattagcaag	gcgtcgttga	ttcgctatgg	tacagcgaca	1740
cacacgggtta	atactgacca	gcgccgcatt	cccctgactc	tgacaaacaa	tggaggaaat	1800
agctattctt	tccaagttcc	tagcgactct	gggtgttgctt	tgcttggtta	ctggatgttg	1860
ttcgtgatga	actcggccgg	tgttcctagt	gtggcttcga	cgattcgcgt	tactcag	1917

<210> 48
 <211> 1917
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Mutant 4.F12 (A1237G, T1650A, T1481C, T1830A) of
 D. Dendroides GaO

gcctcagcac	ctatcggaag	cgccatttct	cgcaacaact	gggccgtcac	ttgcgacagt	60
gcacagtcgg	gaaatgaatg	caacaaggcc	attgatggca	acaaggatac	cttttggcac	120
acattctatg	gcgccaacgg	ggatccaaag	ccccctcaca	catacacgat	tgacatgaag	180
acaactcaga	acgtcaacgg	cttgtctatg	ctgcctcgac	aggatggtaa	ccaaaacggc	240
tggatcggtc	gccatgaggt	ttatctaagc	tcagatggca	caaactgggg	cagccctggt	300
gcgtcaggtg	gttggttcgc	cgactctact	acaaaatact	ccaactttga	aactcgccct	360
gctcgctatg	ttcgtcttgt	cgctatcact	gaagcgaatg	gccagccttg	gactagcatt	420
gcagagatca	acgtcttcca	agctagtctt	tacacagccc	cccagcctgg	tcttggacgc	480
tgggggtccga	ctattgactt	accgattggt	cctgcggctg	cagcaattga	accgacatcg	540
ggacgagtc	ttatgtggtc	ttcatatcgc	aatgatgc	ttggaggatc	ccctgggtggt	600
atcactttga	cgtcttcttg	ggatccatcc	actggtattg	tttccgaccg	cactgtgaca	660
gtcaccaagc	atgatatgtt	ctgccttggt	atctccatgg	atggtaacgg	tcagatcgta	720
gtcacaggtg	gcaacgatgc	caagaagacc	agtgtgtatg	attcatctag	cgatagctgg	780
atcccgggac	ctgacatgca	agtggctcgt	gggtatcagt	catcagctac	catgtcagac	840
ggtcgtggtt	ttaccattgg	aggctcctgg	agcgggtggcg	tatttgagaa	gaatggcgaa	900
gtctatagcc	catcttcaaa	gacatggacg	tccctaccca	atgccaaagg	caacccaatg	960
ttgacggctg	acaagcaagg	attgtaccgt	tcagacaacc	acgcgtggct	ctttggatgg	1020
aagaaggggt	cgggtgttcca	agcgggacct	agcacagcca	tgaactggta	ctataccagt	1080
ggaagtgggtg	atgtgaagtc	agccggaaaa	cgccagtcta	accgtgggtg	agccccctgat	1140
gccatgtgcg	gaaacgctgt	catgtacgac	gccgttaaag	gaaagatcct	gacctttggc	1200
ggctccccag	attatcaaga	ctctgacgcc	acaaccgacg	cccacatcat	caccctcggt	1260
gaacccggaa	catctcccaa	cactgtcttt	gctagcaatg	ggttgtactt	tgcccgaacg	1320
tttcacacct	ctggtgttct	tccagacgga	agcacgttta	ttacaggagg	ccaacgacgt	1380
ggaattccgt	tcgaggattc	aaccccggtg	tttacacctg	agatctacgt	ccctgaacaa	1440
gacactttct	acaagcagaa	ccccaaactcc	attgttcgcg	cctaccatag	catttccctt	1500
ttgttacctg	atggcagggt	atttaacggg	ggtgggtggc	tttgtggcga	ttgtaccacg	1560
aatcatttcg	acgcgcaaat	ctttacgcca	aactatcttt	acaatagcaa	cggcaatctc	1620
gcgacacgtc	ccaagattac	cagaacctca	acacagagcg	tcaaggtcgg	tggcagaatt	1680
acaatctcga	cggattcttc	gattagcaag	gcgtcggtga	ttcgctatgg	tacagcgaca	1740
cacacgggta	atactgacca	gcgcgcgcat	cccctgactc	tgacaaacaa	tggaggaaat	1800
agctattctt	tccaagttcc	tagcgactca	ggtgttgctt	tgccctggcta	ctggatgttg	1860
ttcgtgatga	actcggccgg	tgttcctagt	gtggcttcga	cgattcgcgt	tactcag	1917